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October 1, 2004, 11:56:15; Search time 63.2 Seconds (without alignments) 71.531 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                 US-09-830-779-7
92
1 ROIKIWFQNRRMKWKK 16
                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                      Sequence:
                                                                                             Run on:
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1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	ion
	92	100.0	16	2	AAW45974	A 5 9 7 4	Cyataina
7	92	100.0	16	7	40	340	Dentide 4
m	92	100.0	16	(7	AAW33410	, ,	D-form ne
4	92	100.0	16	~	AAW82958	95	Oestrogen
Ŋ	92	100.0	16	N	AAW56397	Aaw56397	Preferred
φ	92	100.0	16	N	AAW71270	27	Antennane
7	95	100.0	16	C)	AAW71316	Aaw71316	Antennape
æ	92		16	7	AAW30508	Aaw30508	Drosophil
თ	95		16	7	AAW91046	Aaw91046	Internali
10	92	100.0	16	~	AAY52102	Aav52102	Pentide f
11	9	00	16	~1	AAY00859	Aay00859	Peptide p
12	92	100.0	16	N	AAY13509	Aav13509	Signal se
13	92	00	16	m	AAY87920	Aay87920	Drosophil
14	92	00	16	ო	AAB27060	Aab27060	Beta-cate
15	92	00	16	m	AAY93667	Aay93667	Pentide w
16	92	100.0	16	m	AAY67966	Aay67966	Carboxyfl
17	92	00	16	m	AAY93551	Aay93551	Amino aci
18	92		16	m	AAY55818	_	
19	92	00	16	m	AAY71008	Aay71008	Drosophil
50	92	100.0	16	m	AAY51212	Aay51212	
21	92		16	m	AAY51167	Aav51167	Drosophil
22	92	。	16	m	AAB10343	Aab10343	Peptide A
23	92	ö	16	m	AAB19251	Aab19251	Fragment
24	92	0	16	ო	AAY93178	1	Protegrin
25	9		16	m	AAB35694	6	Peptide a

04499007 0007 0007 0007 0007 0007 0007 0	Adu00613 Fruit [1] Adu1205 Membrane Abb78030 Feptide d Abb78214 Amino acid Adu17895 Cell pene Abb78214 Amino acid Adu15616 Drosophil Adu183153 Transloca Abb83153 Transloca Abb83153 Transloca Abb83153 Transloca Abb83153 Transloca Abb83153 Transloca Abb83153 Transloca Abg75500 Fruit [1] Adu785500 Fruit [1] Adu785500 Fruit [1] Adu78500 Antennape Adu783174 Antennape Adu783190 Antennape Adu783190 Fruit[1] Adu783190 Fruit[1] Adu78528 Antennape Adu785128 Antennape Adu785128 Antennape Adu785128 Antennape Adu78512 Fruit[1] Adu78512 Fruit[1] Adu78581 Cell perm Abb96963 Antennape Adu78512 Fruit[1] Adu78512 Fruit[1] Adu78512 Fruit[1] Adu78512 Antennape Adu78312 Human mem Aby7022 Membrane Adu78312 Human mem Aby7022 Membrane Aby7022 Membrane Aby7022 Membrane Aby7022 Membrane Aby7022 Membrane Aby7022 Membrane Aby7023 Membrane Aby703 Membrane Add2315 Antennape	1
AAB220 AAB224 6 3 AAB239 6 3 AAB235 6 3 AAB24 8 3 AAB147 8 4 AAB707 8 4 AAB707 9 4 AAB060 9 4 AAB060	16 4 AAB66996 16 5 ABD78013 16 5 ABD78030 16 5 ABD78030 16 5 AAB78030 16 5 AAB78030 16 5 AAB78031 16 5 AAB78030 16 6 AAB78030 16 6 AAB87803 16 6 AAB78030 16 7 AAB2806 16 7 AAB8603	
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	40 41 42 43 44 45 46 47 48 48 49 49 49 49 49 49 49 49 49 49	

RESULT 2

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This sequence represents a specifically claimed peptide of the formula: V (AAA)n (AAA)n and m = 0-5, totalling 2-5; if n = 1, AAA = ABa; if n = 2, (AAA)n = Gln-AAa; and if n = 3 or more, (AAA)n = (X)D-Gln-ABa; X = any amino acid; p = 1-3, depending on value of n; m = 1, AAA = ARag; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more, (AA2)n = Arg-Gly (X) q; q = 1-3, depending on value of m; v, v' and v', i, any of which may be absent, agent able to direct the compound to a specific of which may be absent. = agent able to direct the compound to a specific of which peptides are inhibitors of cysteane proteases, specifically interleukin-1 beta converting enzyme (ICB). They inhibit death of cells, particularly in humans, and can be used to treat neurodegenerative
 Aab13424 Synthetic
Ade14787 Carrier m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases (e.g. ageing, Alzheimer's, Machado-Joseph, Parkinson's or Huntington's diseases, multiple sclerosis, muscular dystrophy, stroke), cardiovascular disease and liver disorders. The peptides should be more specific than pseudosubstrate inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cysteine protease inhibiting peptide(s) for preventing cell death -
in cases of neuro; cagenerative, cardiovascular and liver diseases, and
their peptido:mimetics, and general method for identifying enzyme
inhibiting peptides.
                                                                                                                                                                                                                                                      Cysteine protease inhibiting peptide for preventing cell death.
                                                                                                                                                                                                                                                                                     Neuronal cell death; neurodegenerative disorder; inhibition; cysteine protease; cardiovascular; liver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 92; DB 2; Length 16; 100.0%; Pred. No. 8.6e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"
                                                                   ALIGNMENTS
 AAB13424
ADE14787
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                      AAW45974 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 68; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCO ) UNIV COLUMBIA NEW YORK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US004158.
   ოო
                                                                                                                                                                                                                        (first entry)
   17
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Best Local Similarity
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-1997.
                                                                                                                                                                                                                        01-JUL-1998
 92
                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                       AAW45974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Troy CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                    RESULT 1
AAW45974
99
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New peptides are provided which are 16 amino acids long and which are analogues of the peptide corresponding to residues 43-58 of the Antennapedia transcription factor homeodomain (AntpHD). The peptides contain 6-10 hydrophobic amino acids. They have the general formula: X1-X2-X3-X4-X5-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-X12-X11-X10-X9-X8-X7-TTD-X5-X4-X13-X1-X16-X16-X15-X16 are any alpha-amino acids, provided that: (1) the peptide contains 6-10 hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the natural Antp 43-85 sequence RQIKINFONRRAWKK (i.e. the present sequence) is excluded. Specific examples of these peptides are given in AAW33416. The peptides are used as vectors for introducing into live acids. They can cross cellular membranes and reach various cell
                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide(s) of high hydrophobic amino acid content - useful as vectors for delivering peptides and nucleic acids to cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                   homeodomain; transcription factor; Antennapedia; Antp; vector; transfection; hydrophobic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 92; DB 2; Length 16; 100.0%; Pred. No. 8.6e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compartments. They are as effective as helix (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-form peptide 43-58 of homeodomain Antp.
              AAW33407 standard; peptide; 16 AA.
                                                                                                                     Peptide 43-58 of homeodomain Antp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW33410 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                      (CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 7; 35pp; French.
                                                                                                                                                                                                                                                                                                                        95FR-00011714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RQIKIWFQNRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                    Prochiantz A;
                                                                        (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-226166/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 AA;
                                                                                                                                                                                                                               WO9712912-A1.
                                                                                                                                                                                                                                                                                           04-OCT-1996;
                                                                                                                                                                                                                                                                                                                        35-OCT-1995;
                                                                        27-AUG-2003
17-MAR-1998
                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                      Chassaing G,
                                                                                                                                                                                                                                                             .0-APR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                            AAW33407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AAW33407
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homeodomain; transcription factor; Antennapedia; Antp; vector;

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Gaps

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1 ROIKIWFONRRMKWKK 16 ROIKIWFONRRMKWKK 16

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16; Conservative

Synthetic

WO9712912-A1

10-APR-1997

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The present invention describes a composition comprising an isolated oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The peptides used in the composition comprise sequences of human oestrogen receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1 (SCR-1). The peptide compositions, nucleic acids and vectors of the present invention can reduce OR activity in a cell, reduced OR polypeptide dimerisation in a cell and reduce the binding of SRC-1 polypeptide to an OR polypeptide dimer in a cell. They can be used for killing cancer cells and treating cancers, particularly breast cancer. The present sequence represents a specifically claimed anti-oestrogen peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal peptide; nuclear localisation signal; NLS; immunosuppressive activity; inhibition; nuclear translocation inhibitor; nuclear translocation; treatment; immune disorder; autoimmune disease; hypersensitivity; sepsis; prevention; septic shock; antiviral agent;
                                                                                                                                                                                                                                                                                                                                                         New anti-oestrogen peptide compositions - comprise sequences based on oestrogen receptor and steroid receptor co-activator-1 sequences, used for treating cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 92; DB 2; Length 16
100.0%; Pred. No. 8.6e-07;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preferred signal sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 59; Page 156; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW56397 standard; peptide; 16 AA.
                                                                                                                                         98WO-US007711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                 WPI; 1998-594522/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 AA;
         Homo sapiens.
                                                 WO9846250-A1.
                                                                                                                                         14-APR-1998;
                                                                                                                                                                                   14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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12-SEP-1997;
                                                                                             22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-1998,
                                                                                                                                                                                                                                                                       Pietras RJ:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides are provided which are 16 amino acids long and which are analogues of the peptide corresponding to residues 43-58 of the analogues of the peptide corresponding to residues 43-58 of the Antennapedia transcription factor homeodomain (Antphi). The peptides contain 6-10 hydrophobic amino acids. They have the general formula: X1-X2-X1-X4-X5-XTP-XX-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any alpha-amino acids, provided that: (1) the peptide contains 6-10 hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the cather amino acids; (4) Peptides are specific or actural Antp As 58 sequence ROINIWPONREWINKIK (see ANW33407) is excluded. The present sequence (the D-form of the 43-58 peptide) is a specific example of the new peptides. The peptides are used as vectors for introducing into live cells compounds which affect cell function, especially peptides and nucleic acids. They are as effective as helix 3 of a homeodomain peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                     Incte= "in determining the ability of this sequence to be internalised in cells, a biotin-aminopentanoyl group was attached to the N-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide(s) of high hydrophobic amino acid content - useful as vectors for delivering peptides and nucleic acids to cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis; breast cancer; estrogen; tumour; phosphotyrosyl peptide; malonyltyrosyl peptide; steroid receptor co-activator-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                    Location/Qualifiers
1. .16
/note= "all residues are D-form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW82958 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 7; 35pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                        (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                              95FR-00011714.
                                                                                                                                                                                                                                                                                                                                                       96WO-FR001553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prochiantz A;
transfection; hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-226166/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                    Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16 AA;
                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chassaing G,
                                                                                                                                                                                                                                                                                                                                                    04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1995;
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Gaps

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(BRIM) BRISTOL-MYERS SQUIBB CO.

04-FEB-1999

q ઠે

Synthetic

Length 16;

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contribution numbers to represent presents asymptomes and presents of the invention. They are used to construct the nuclear translocation inhibitor polypeptides of the invention. Nuclear translocation inhibitor conjugates a signal sequence peptide capable of delivering the polypeptide comprise a signal sequence peptide capable of delivering the polypeptide through the cytoplasmic membrane into a cell, and at least 2 nuclear localisation signals. The polypeptides can be used to inhibit nuclear translocation of a cellular protein. In addition, since the nuclear translocation of certain cellular peptides is required for the host organism to mount an immune response, the polypeptide for the host organism to mount an immune response, the polypeptides can therefore be used for the treatment of immune disorders including autoimmune diseases. The polypeptides can therefore be used for the treatment of immune disorders including autoimmune diseases. The polypeptides can also be used for treating physical symptoms manifested by responses to allergens which can initiate a state of hypersensitivity, for the treatment of sepsis and in the prevention of septic shock, antiviral agents, tumour growth suppressors, and for septic shock, antiviral agents, tumour growth suppressors, and for transcriptionally modulating the expression of cellular genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                      nuclear translocation inhibitor polypeptides - comprising signal sequence for delivery through the cytoplasmic membrane and at least 2 nuclear localisation sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense oligonucleotide; inhibit; cell death; Nedd2; human Ich-1L gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antennapedia peptide for directing antisense oligonucleotides to a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuronal cell death, treatment, aging, amyotrophic lateral sclerosis; Alzheimer's disease, dentatorubral, pallidolyusial atrophy; Huntington's disease, Machoado-Joseph disease, multiple sclerosis; muscular dystrophy, Parkinson's disease; senility; spinocerebellar ataxia type I; spinobulbar muscular atrophy; stroke; trauma; antennapedia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-terminal protected with 3-nitro-2-pyridyl sulphenyl group (NpyS)"
                                                                                                                                                                                           AAW56397-99 represent preferred signal sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 92; DB 2; Length 16; 100.0%; Pred. No. 8.6e-07;
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Haffar OK;
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Blake J,
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                                                                                                                                                         Claim 5; Page 43; 69pp; English.
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  Cleaveland
                                     WPI; 1998-217028/19.
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Best Local Similarity
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Modified-site
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    Nadler SG,
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Matches
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AAW71270
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                                                                                                                                                   AAW71270 and AAW71315-16 represent antennapedia peptides which are used to, direct the antisense oligomucleotides (AAV54973-4) of the invention to a cell. The antisense oligomucleotides are used to inhibit cell death mediated by withdrawal of a trophic factor. AAV54974 inhibits the expression of a Nedd2 rodent gene, while AAV54974 inhibits expression of a human Ich-IL gene. The oligomucleotides are used to inhibit neuronal a human Ich-IL gene. The oligomucleotides are used to inhibit neuronal cell death, especially for treatment of neuronal cell death caused by e.g. aging, amyotrophic lateral sclerosis, Alzheimer's disease, Machoadodentatorubral and pallidolyusial atrophy, Huntington's disease, Machoadodoseph sensility, spinocerbellar ataxia type I, spinobulbar muscular atrophy, stroke or trauma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antennapedia peptide for directing antisense oligonucleotides to a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                         Anti-sense oligonucleotide(s) to cysteine aspartase genes - used to inhibit neurodegenerative disorder associated with e.g. ageing, Alzheimer's, Huntington's or Parkinson's disease.
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                                                                                                                                 Claim 5; Page 39; 60pp; English
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Best Local Similarity 100.
Matches 16; Conservative
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Troy CM, Shelanski ML;
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                                WPI; 1998-506333/43
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 AA;
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Modified-site
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AAW71270 and AAW71315-16 represent antennapedia peptides which are used to, direct the antisense oligonucleotides (AAV54973-74) of the invention to a cell. The antisense oligonucleotides are used to inhibit cell death mediated by withdrawal of a trophic factor. AAV54973 inhibits the expression of a Nedd2 rodent gene, while AAV54974 inhibits expression of a human Ich-IL gene. The oligonucleotides are used to inhibit neuronal cell daath, especially for treatment of neuronal cell dath, especially for treatment of neuronal cell dath, amyotrophic lateral sclerosis, Alzheimer's disease, dachoado-Joseph disease, multiple sclerosis, muscular dystrophy, Parkinson's disease, sanility, spinocerebellar ataxia type I, spinobulbar muscular atrophy, stroke or trauma
Anti-sense oligonucleotide(s) to cysteine aspartase genes - used to inhibit neurodegenerative disorder associated with e.g. ageing, Alzheimer's, Huntington's or Parkinson's disease.
                                                                                                          Disclosure; Page 14; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16 AA;
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100.0%; Score 92; DB 2; Length 16; 100.0%; Pred. No. 8.6e-07; Live 0; Mismatches 0; Indels 16 ROIKIWFONRRMKWKK 16 1 ROIKIWFONRRMKWKK Best Local Similarity 100. Matches 16; Conservative ò

Query Match

AAW30508 standard; peptide; 16 RESULT 8 AAW30508

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26-OCT-1998 AAW30508;

Drosophila membrane translocation sequence.

DP-1; transcription factor; antagonist; E2F protein; apoptosis; cell proliferation; cardiovascular cell; restenosis; tumour; surgical stent; therapy; membrane translocation; antennapedia protein.

Drosophila melanogaster.

WO9828334-A1.

02-JUL-1998.

97WO-GB003506 22-DEC-1997;

96GB-00026589 20-DEC-1996;

(PROL-) PROLIFIX LTD.

Bandara LR; La Thangue NB,

WPI; 1998-377596/32.

Polypeptide fragments of the DP-1 transcription factor - used for inducing apoptosis, specifically in tumour and cardiovascular cells, e.g. for preventing re-stenosis.

Disclosure; Page 5; 55pp; English.

the Drosophila melanogaster antennapedia protein. Such membrane translocation sequences are useful in directing entry of a polypeptide into a cell. Polypeptides of the invention (see AAW3064-07) are derived from the DEF box region (see AAW30601) of transcription factor DP1. They act as antagonists of the heterodimerisation of a DP protein with an E2F protein, and can be used to induced apoptosis, specifically in tumour and This polypeptide comprises a membrane translocation sequence derived from

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cardiovascular cells, e.g. for preventing restenosis. A claimed fusion protein comprises a DEF box peptide and the Drosophila antennapedia protein membrane translocation sequence
                                                                                                              Gaps
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                                                                                    Length 16;
                                                                                Score 92; DB 2; I
Pred. No. 8.6e-07;
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                                                                              Query Match
Best Local Similarity
Matches 16; Conserv
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AAW91046 standard; peptide; 16 AA. RESULT 9

AAW91046;

24-MAR-1999 (first entry)

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Gaps

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Internalization sequence associated with cadherin modulating agents.

Alpha-catenin; beta-catenin; interaction; modulation; cell adhesion; cadherin-mediated function; demyelinating neurological disease; multiple sclerosis; drug delivery; cancer; angiogenesis; immune system; central nervous system; apoptosis induction; cadherin-expression cell; pregrancy prevention; vasopermeability; synaptic stability; diabetes; rheumatoid arthritic; allergic response; learning; antennapedia protein; antibody-mediated graft rejection; internalization sequence; memory.

Synthetic.

WO9845319-A2

15~OCT-1998

98WO-CA000322 14-APR-1998; 97US-0043361P 10-APR-1997;

(UYMC-) UNIV MCGILL.

Gour BJ; Blaschuk OW,

WPI; 1999-024009/02.

New catenin modulating agents - comprising peptides having a sequence HAV or analogues or antibodies, used for modulating cadherin-mediated functions

Claim 16; Page 78; 106pp; English.

The present sequence represents antennapedia protein derived
internalization sequence associated with cadherin modulating agents.
These agents are used for modulating cadherin-mediated functions. They
can be used for disrupting interaction between alpha-catenin and betacatenin in a cell, inhibiting cell adhesion, e.g. between epithelial
cells, endochelial cells, neural cells, tumour cells and lymphocytes,
treating a demyelinating neurological disease, e.g. multiple sclerosis,
for reducing unwanted cellular adhesion in a mammal, for enhancing the
delivery of a drug through the skin of a mammal, for enhancing the
delivery to the central nervous system of a mammal, for thanding drug
delivery to the central nervous system of a mammal, for inducing
cells and cadherin-expression cell, for modulating the immune system
of a mammal, for preventing pregnancy in a mammal, for increasing
vasopermeability in a mammal, or for inhibiting synaptic stability in a
mammal In particular they can be used for treating diabetes, rheumatoid
arthritic, allergic responses, antibody-mediated graft rejection or for
stimulating learning and memory

ROIXIWFONRRMKWKK 16 1 ROIKIWFONRRMKWKK 16

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AAY00859 standard; peptide; 16 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a peptide from the third helix of the Drosophila antennapedia protein that translocates across biological membranes. This sequence can be linked to the Rho binding region of the invention (AAYS100) to cause translocation across eukaryotic cell membranes. The Rho binding region is present in many Rho binding proteins, such as ROCK-IT and Kinectin and is also referent to as the ROCK/Kinectin monology domain. Rho-A is involved in many cellular processes including stress fibre formation, cell motility, cytckinesis and apoptosis. The Rho binding domain is used in the invention which relates to an assay for potential modulators of cell growth. The assay consists of a Skn7 polypeptide, a beraz polypeptide on a polypeptide consisting of a rock/Kinectin homology domain, a Rho polypeptide which binds to the previous peptide and a test compound. The modulation of the heathed is used to identify modulators, particularly antagonists, of the interaction control the host's defence system, particularly as antifungal agents. The Rock host's defence system, particularly as antifungal agents. The Rock host is defence system, particularly as antifungal agents. The Rock host is controled by the test compound to screen databases for other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assay for modulators of binding of Rho protein with its binding partners, potentially useful as antifungal agents.
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Rho binding region; Rho binding protein; ROCK II; ROCK I; Kinectin; ROCK/Kinectin homology domain; cell growth; assay; Skn 7; modulator; antifungal agent; antennapedia homeodomain protein; translocate.
                                                                                                                                                                                                                                                                                                                                                                               Peptide from the third helix of antennapedia homeodomain protein.
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                                                100.0%; Score 92; DB 2; Length 16; 100.0%; Pred. No. 8.6e-07; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.6e-07;
.ive 0; Mismatches 0; Indels
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(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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                                                                                                                                                                                                                                                                   . AAY52102 standard; peptide; 16 AA
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                                                                                           16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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SQ Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New membrane-permeable constructs - comprise a peptide linked by a labile bond to a nucleic acid analogue capable of hybridising with an intracellular polynucleotide.
                                                                                                                                               Membrane-permeable construct; lipid membrane; membrane transport; oligonucleotide delivery; cancer therapy; signal transduction; inhibitor; gene therapy; transcription; translation; expression; replication.
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                                                                                                                   Peptide pAntp(43-58) used in membrane-permeable construct.
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                                                                                                                                                                                                                                           Location/Qualifiers
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Modified-site
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AAY13509 ID AAY13509 standard; peptide; 16 AA.

Gaps

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Conservative

97US-00964614.

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Mutant forms of mammalian Rad51 proteins and polypeptides that disrupt cell proliferation and promote programmed cell death, encoded by specific nucleotides.
                              Rad51, cell proliferation, rad51TR1-131; rad51K-A134; immunosuppressive; cytostatic; antiinflammatory; antiproliferative; programmed cell death; treatment; autoimmune disorder; inflammation; cancer; graft rejection; proliferative disorder; hyperproliferative disorder; antennapedia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Col 31-32, 22pp, English.
                                                                                                                                                                                                                                                                                                                                   (LEXI-) LEXICON GENETICS INC
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                                                                                                                                  Drosophila sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention features fusion proteins that contain a calpastatin peptide and a signal sequence capable of delivering the fusion protein into a calcardate of the contains are specifically used; (a) to prevent in a cell. The fusion protein is used for the inhibition of calpain in a cell. The fusion proteins are specifically used; (a) to prevent capacity of delibrating subsequent transfusion of patelets (e.g. during storage); (b) to inhibit thyoxia-induced sickling of erythrocytes (during storage); (b) to inhibit actions storage); (c) to inhibit activation of human immune sickle cell crises); and (c) to inhibit activation of human immune of sickle cell crises); and (c) to inhibit activation of human immune viruses regulated by NP-kapabab. Other disclosed uses are: to treat or viruses regulated by NP-kapabab. Other disclosed uses are: to treat or prevent inflammation (e.g. arthritis or asthma), unwanted immune corresponses (e.g. transplant rejection), restenosis (associated with angioplasty), cancer, subarachnoid hemorrhage, vasospass, muscular dystrophy, cancer, subarachnoid hemorrhage, vasospass, defents, catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis in by-pass surgery and catheters etc.); to reduce coronary thrombosis, to prevent progression of infarction (myocardial infarction, or to prevent progression of thinbitory effec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                         Fusion protein; calpastatin; calpain; platelet aggregation; arthritis; hypoxia; erythrocyte sickling; sickle cell; HIV provirus; NF-kappaB; inflammation; asthma; immune response; restenosis; myocardial infarction; cancer; calpastat; antennapedia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusion protein of signal sequence and calpastatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 92; DB 2; I 100.0%; Pred. No. 8.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stored cold with reduced change in shape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 5; 46pp; English.
                                                                                                  Signal sequence of antennapedia.
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                                                                                                                                                                                                                                                                                                                                                                                                        97US-00964302
                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potter DA, Skolnik PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-326923/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 AA;
                                                         30-JUL-1999
                                                                                                                                                                                                                                                                                    WO9922756-A1
                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                          04-NOV-1997;
                     AAY13509;
                                                                                                                                                                                                                                           Mammalia.
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Best Local S
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This invention describes novel truncated and altered forms of RadSiproducts encoded by radSiTR1-131 and radSiK-A134. The products of the invention have immunosuppressive, cytostatic, antiinflammatory and antiproliferative activity. Altered and mutant forms of RadSi are useful for inhibiting cell proliferation and for promoting programmed cell death. Therapeutic agents, factors or compounds capable of disrupting the essential processes mediated by or associated with normal RadSi or RadSZ cancer, graft rejection and other proliferative and hyperproliferation, disorders. This sequence represents a fragment of the Drosophila antennapedia protein which is described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-catenin, cadherin-mediated intercellular adhesion, cell differentiation, modulating agent, hair loss, skin exfoliation, internalisation moiety, flanking sequence, transcription, hearing loss.
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-catenin derived internalisation moiety SEQ ID NO: 47.
                                                                                                                                                                                                                                                                                                                       Length 16
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                100.0%; Score 92; DB 3; I
100.0%; Pred. No. 8.6e-07;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        1 ROIKIWFONRRMKWKK
                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                           Sequence 16 AA;
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Drosophila sp. antennapedia protein fragment.

(first entry)

11-SEP-2000

AAY87920

AAY87920 ID AAY8 XX AAY8 XX II-¢ XX DT II-¢ XX DE DEO6

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AAY87920 standard; peptide; 16

1 ROIKIWFONRRMKWKK 16 ROIKIWFONRRMKWKK 16

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RESULT 16
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                                                                                                                                                                                                              The present invention is concerned with methods of modulating the amount of free beta-catenin in the cell, and methods of stimulating the expression of genes involved in cellular differentiation, the transcription of which is under the control of beta-catenin. The peptides given in AABZ7053-B27084, B27350 and AABZ732-B27351 can be used beta catenin, causing increased levels of the latter and stimulating the activation of beta-catenin mediated transcription. This can be used to stimulate cell differentiation, which can then be used to promote hair growth and skin exfoliation. This latter is particularly useful in the mimorovement of photocatanged skin and to mimise wrinkles. The modulating peptide can also be used to reduce hearing loss resulting from inner ear disorders such as hyperacusis and tinnitus
                                                                                                                Stimulating beta-catenin mediated gene expression, cellular differentiation and hair growth, involves contacting cells with modulating agent capable of inhibiting interaction between alpha and beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anticancer agent; cancer cell; resistance; P-glycoprotein pump; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 92; DB 3; Length 16; 100.0%; Pred. No. 8.6e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Temsamani J, Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY93667 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                        Claim 8; Page 38; 77pp; English.
99US-00265107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ROIKIWFONRRMKWKK 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                        Blaschuk OW, Gour BJ;
                                                                                   WPI; 2000-594308/56.
                          (UYMC-) UNIV MCGILL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200032237-A1.
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                             catenin.
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The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport if into canner cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be passive mechanism (no receptors required), and are non-toxic and nonlytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a cell permeable peptide comprising at least the hydrophobic core of a signal peptide (or analogue) containing at least 1 additional positively charged amino acid (or analogue). The peptides are useful for the intracellular delivery of molecules, especially peptide nucleic acids to in vivo targets. The peptides are useful in commercial drug-delivery systems, in e.g. gene therapy, cancer therapy and anti-infectious agent therapy. The peptides facilitate biochemical and molecular biological research. The modified peptides facilitate intracellular delivery of any cell-impermeable substances and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cell permeable signal peptides, useful for intracellular delivery of a molecule.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karposi syndrome; fibroblast growth factor; signal peptide; PNA; peptide nucleic acid; cell permeability; intracellular delivery; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 92; DB 3; Length 16; 100.0%; Pred. No. 8.6e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note≈ "labelled with carboxyfluorescein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carboxyfluorescein cell permeant peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY67966 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nelson J, Harriott P, Wallace A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 29; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 ROIKIWFONRRMKWKK 16
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                         Sequence 16 AA;
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                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY67966;
                                                                                                                                                                                                                                                                                                                                      Query Match
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Cellular protein, nuclear translocation; nuclear localization signal; immunosuppressant; immune response; viral infection; immune disorder; rheumatoid arthritis; multiple sclerosis; juvenile-onset diabetes; NLS; systemic luque eryrematosus; SLE; asthma; sepsis; tumor growth; fibroblast growth factor; signal sequence.

Signal segeunce for delivering polypeptide inhibitor.

(first entry)

06-MAR-2000

AAY55818;

AAY55818 standard; peptide; 16

AAY55818

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein transduction system for treating cancer and pathogenic infections has a fusion protein comprising a protein transduction domain covalently
improve delivery into low permeability cells. Delivery into sub-
compartments can be achieved by modifying the signal peptides. The
present sequence represents a peptide used in the exemplification of the
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a synthetic protein transduction domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is also useful for treating cancer, especially prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein transduction system; protein transduction domain; cytotoxic domain; pathogen infection; retroviral infection; plasmodial infection; cancer; prostate cancer.
                                                                                                                            Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 92; DB 3; Length 16; 100.0%; Pred. No. 8.6e-07; ive 0; Mismatches 0; Indels
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0
                                                                                                                         Score 92; DB 3; I
Pred. No. 8.6e-07;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                               AAY93551 standard; peptide; 16 AA.
                                                                                                                       100.0%; Sc
100.0%; Pr
tive 0;
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linked to a cytotoxic domain.
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                 Query Match
Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity
                                                     present invention
                                                                                      Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200034308-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                AAY93551;
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8888888
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Novel composition comprising a nuclear localization signal and an inhibitor of nuclear translocation, useful for preventing transplanted

organ or tissue rejection.

WPI; 2000-062141/05.

Nadler SG;

(BRIM) BRISTOL-MYERS SQUIBB CO.

99WO-US008984

26-APR-1999; 04-MAY-1998;

W09957138-A1.

Synthetic.

11-NOV-1999.

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The invention provides a composition comprising an isolated polypeptide (I) (polypeptide inhibitor of a cellular protein nuclear translocation) which comprises a signal sequence peptide capable of delivering (I) through a cytoplasmic membrane into the cell; and a nuclear localization signal sequence (NLS) present along with an immunosuppressant. (I) or its derivatives provide useful tools for introducing an exogenous polypeptide comprising an NLS into an intact cell to inhibit nuclear translocation of a cellular protesion, for studying the role of nuclear translocation in the regulation of cellular processes. See AAVSS812 for detailed uses of (I) and compositions contianing (I). The present sequence represents a signal sequence for delivering the (I) through the cytoplasmic membrane into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 8.6e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila antennapedia (ANT) transport peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 14; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY71008 standard; peptide; 16 AA.
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100.0%; P2
tive 0;
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16 AA;
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AAY71008
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AC AAY7
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16

ROIKIWFONRRMKWKK

1 ROIKIWFONRRMKWKK 16

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16, Conservative

Best Loca Matches

99EP-00112544. 98DE-01029495

01-JUL-1999; 02-JUL-1998;

05-JAN-2000.

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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPASE (SERCA2A) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against CLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2A interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the transport peptide composed of tresidues 41-58 of antennapedia (MNT), a drosophila transport transcription factor protein. This peptide can be used to transport transcription agents across a cell membrane into the cytoplasm and nucleus
Phospholamban, PLB, sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiomyocyte; transport peptide, penetratin; cargo peptide, inhibitor; contractilin; cardiac contractility; cardiac disease; antennapedia; ANT; treatment; cardiant; heart failure; myocardial dysfunction; fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                      Hoshijima M, Meyer M;
                                                                                                                                                                                                                                                                                                                                                        He H,
                                                                                                                                                                                                                                                                                                                                                        Minamisawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 50; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Silverman GJ;
                                                                                                                                                                                                                    99WO-US025692
                                                                                                                                                                                                                                                         98US-0106718P
99US-0145883P
                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                        Dillman W,
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-365393/31.
                                                                                                                                                                                                                                                                                                                                                                             Wang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of cardiomyocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   triphosphatase.
                                                                                                                                            WO200025804-A2
                                                                                                     Drosophila sp.
                                                                                                                                                                                                                    02-NOV-1999;
                                                                                                                                                                                                                                                            02-NOV-1998;
                                                                                                                                                                                                                                                                                27-JUL-1999;
                                                                                                                                                                               11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                        Chien K,
Scott C,
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Fluorogenic conjugate for intracellular fluorescence labeling, especially for performing fluorescence resonance energy transfer assays in living cells.

WPI; 2000-099447/09 Paysan J, Antz C; (PAYS/) PAYSAN J. (ANTZ/) ANTZ C.

Claim 5; Page 5; 8pp; German.

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This invention describes a novel fluorogenic conjugate (vector) for fluorescence labeling of specific targets within cells which comprises a membrane translocation component, a targeting component and a fluorophore. A kit comprising two such conjugates; in which the fluorophores form a donor-acceptor pair for fluorescence resonance energy transfer (FRET), can be used to messure interactions between two component of the conjugates targets one of the substances and the targeting component of the conjugates targets one of the substances and the targeting component of the other conjugate targets the other substance. The conjugate to messure interactions between the targeting component of the other conjugate has a fluorophore capable of acting as a donor or acceptor for FRET with a fluorescent protein, it can be constant and cell. When the conjugate has a fluorophore capable of acting as a donor or acceptor for FRET with a fluorescent protein, it can be the functed by FRET if the targeting component targets a sequence fluorescent protein, especially in a screening assay in which the gene fluorescent protein, especially in a screening assay in which the cells are separated, preferably by means of a cell sorter or by FRET care separated, preferably by means of a cell sorter or by FRET care separated, preferably by means of a cell sorter or by FRET care separated, preferably by means of a cell sorter or by FRET capacitic blue or AMCA. The cells are especially bacterial, yeast, insect, amphibian or mammalian cells. This sequence represents a fragment of the function which is used to illustrate the method are the factor of the method of a cell sorter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY51212 standard, peptide; 16 AA
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Gaps

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Length 16;

100.0%; Score 92; DB 3; Length 16 100.0%; Pred. No. 8.6e-07; ive 0; Mismatches 0; Indels

Conservative

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TAT protein; nuclear transport; cell adhesion; gene therapy.
                                                                                                                                                                                      Drosophila sp. derived peptide fragment.
                                                                                                     AAYS1167 standard; protein; 16 AA.
1 ROIKIWFONRRMKWKK 16
                            1 ROIKIWFONRRMKWKK 16
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                 Drosophila sp.
                                                                                                                                                                                                                                                                               WO9966061-A1.
                                                                                                                                                             31-MAR-2000
                                                                                                                                 AAY51167;
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IID AAYE
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XX XX TAT
XX XX YA WO99
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Antennapedia, homeodomain, fluorogenic, fluorescence, fluorophore, fluorescence resonance energy transfer, FRET; detection.

EP969284-A1.

Antennapedia protein homeodomain peptide fragment 1.

(first entry)

04-APR-2000

EXSXEXEXEXSXE

AAY51212

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Gaps

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activity which comprise a nuclear localization sequence and a fragment of the retinoblastoma protein. The products of the invention have antitumor, antipporial antipporial antipporial antipporial antipporial antipporial antipporial antipporial antipporial and protein antipporial and protein antipporial and or hyperprofileration of cells, specifically benign or malignant tumors (sepecially of the breast), atherosclerosis and psoriasis. (I) are more active against proliferation than similar reduced, thus also reducing the cost. They destroy amost all types of tumor cells, especially those in which the retinoblastoma gene or protein is defective, but have relatively ittle effect on normal cells, which is in contrast to conventional chemotherapeutic agents. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a fragment of the Antennapedia protein (amino acids 43-58) from Drosophila. The fragment is used as a translocating protein in the course of the invention. The specification describes a method for modulating cellular process and for delivery of functional protein sequences. The method comprises contacting a cell in culture under suitable conditions with a cell process modifying molecule attached to a translocating polypeptide, where molecule is translocated into the cell and interacts specifically with a responsive target site. The method is useful for modulating a cellular process, such as modulating expression of a target gene product, of a cell in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating a cellular process by contacting a cell in culture with a process modifying molecule attached to a translocating polypeptide, useful for modulating expression of a target gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antennapedia protein; translocating protein; cellular process;
                                                                                                                                                                                                                                                                                           100.0%; Score 92; DB 3; Length 16; 100.0%; Pred. No. 8.6e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragment of the Antennapedia protein from Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 6; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB19251 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000, 2000WO-US008571.
                                                                                                                                                                                                                                                                                                                                                                1 ROIKIWFONRRMKWKK 16
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                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-611716/58.
                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein delivery.
                                                                                                                                                                                                                                                            Seguence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-0CT-2000
                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB19251;
                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antiproliferative, nuclear localization sequence, retinoblastoma protein, antitumor, antipsoriatic, antiatherosclerotic, treatment, diagnosis, benign tumor, malignant tumor, breast, atherosclerosis; psoriasis;
                                                                                                                                                                                                                                                                                                    This invention describes a novel phage whose head part contains a bifunctional protein with nuclear transport and cell adhesion activities. The phage is used as a vector for transport of foreign genes into a cell nucleus for gene therapy. This sequence represents a peptide fragment which is used in the method of the invention
                                                                                                                                                                                                                    carrying in its head part a bifunctional nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel peptides (I) with high antiproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide with high antiproliferative activity, useful for treating cancer or psoriasis, comprises a nuclear localization sequence and a fragment of the retinoblastoma protein.
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                                                                                                                                                    Nakanishi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                    Наведама М,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 92; DB
Pred. No. 8.6e
; Mismatches
                                                                                                                                                   Takeda K,
                                                                                                                                                                                                                                                                     Disclosure; Page 38; 42pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB10343 standard; protein; 16 AA.
                                                                                                                                                                                                                  Phage for gene therapy carrying transport/cell adhesion protein.
                                                                                                                                                   Okuyama H,
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                                                 99WO-JP003272.
                                                                               98JP-00189845.
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                (DNAV-) DNAVEC RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RADU/) RADULESCU R T.
                                                                                                                                                                                  WPI; 2000-097750/08
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                                                                                                                                                   Yokoi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide AB fragment.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 AA;
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                                             18-JUN-1999;
                                                                               18-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemotherapy
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              23-DEC-1999
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The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) XI-XI6; (b); BXXBXXXXBBXXXXXBBXXXXBBXB, where: each of XI-XI6 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be and each X is an aliphatic or aromatic a. The linear peptide may be retro forms of (a)-(c) containing D- and/or L-form as dragment containing at least 5, preferably at least 7 consecutive as fragment containing at least 5, preferably at least 7 consecutive as fragment exchyplesins, transportan, etc. Of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main categories based on their structure: (i) peptides with alpha-helices, e.g. protegrin, tachyplesins, defensins; (ii) peptides with alpha-helices of e.g. bactericins and PR39. The peptides of the invention fall into the peptide antibiotic categories defensins; (iii) peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Rotchylesins. This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                       analgesic; antimicrobial;
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                       Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrol blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyelin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "linked to doxorubicin via a succinimydyl
maleimido-propionate-3-mercaptopropionate linker"
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 Length 16;
                                   0; Indels
 Score 92; DB 3; I
Pred. No. 8.6e-07;
                                       Mismatches
                                                                                                                                                                                                                                                                                                                     Protegrin-like peptide antibiotic No 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                         AAY93178 standard; peptide; 16 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example I; Page 13; 54pp; French,
                                       .
ch 100.0%;
l Similarity 100.0%;
16; Conservative 0
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                                                                          ROIKIWFONRRMKWKK 16
                                                                                                              1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYNT-) SYNT: EM SA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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   Query Match
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Matches 16
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                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alization molety and a peptide,
transcription and cell
for inhibiting Alzheimer's
                                                                                                                                     ü
represents a synthetic linear peptide designed on peptides able to crothe BBB and is conjugated to a doxorubicin molecule by a succinimydyl maleimido-propionate-3-mercaptopropionate linker. Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide associated with modified beta-catenin expression #27.
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                                                                                                                                                                                                                                                                          Length 16;
                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                            100.0%; Score 92; DB 3; I 100.0%; Pred. No. 8.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB35694 standard; peptide; 16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ADHE-) ADHEREX TECHNOLOGIES INC.
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Matches 16; Conser
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                                                                                                                                                                         BBB models
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Search completed: October 1, 2004, 12:13:07 Job time : 69.2 secs

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October 1, 2004, 12:07:51; Search time 17 Seconds (without alignments) 48.589 Million cell updates/sec
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1: \cgn2_6\ptodata2/\iaa/5A_COMB.pep:*
2: \cgn2_6\ptodata2/\iaa/5B_COMB.pep:*
3: \cgn2_6\ptodata3/\iaa/6A_COMB.pep:*
4: \cgn2_6\ptodata3/2\iaa/6B_COMB.pep:*
5: \cgn2_6\ptodata3/2\iaa/FB_COMB.pep:*
6: \cgn2_6\ptodata3/2\iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 100 summaries
                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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92
1 RQIKIWFQNRRMKWKK 16
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	ecunentes ecuentes ec
RIES	US-08-928-958-7 US-08-810-540-3 US-09-072-429-7 US-09-072-429-6 US-09-116-294-4 US-09-116-294-4 US-09-116-294-4 US-09-204-6143-4 US-09-204-66-54 US-09-208-96-5-4 US-09-208-96-5-4 US-09-208-96-5-4 US-09-208-96-33 US-09-208-96-33 US-09-308-210 US-09-308-210 US-09-308-210 US-09-308-310 US-09-308-310 US-09-308-310 US-09-308-310 US-09-308-310 US-09-308-310 US-09-310-310 US-09-310-310 US-09-310-310 US-09-310-310 US-09-310-310 US-09-310-310 US-09-310-310 US-09-311-310 US-09-31-310 US-09-31-310 US-09-31-31-310 US-09-31-31-310 US-09-31-31-31-31 US-09-31-31-31-31 US-09-31-31-31-31 US-09-31-31-31-31 US-09-31-31-31-31 US-09-31-31-31-31 US-09-31-31-31-31-31 US-09-31-31-31-31-31 US-09-31-31-31-31-31-31 US-09-31-31-31-31-31-31-31-31-31-31-31-31-31-
DB	; ; QQQQAAAAAA ;
Length	
Score	
Result No.	11111111111111111111111111111111111111

Sequence 47, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 27,
US-09-265-107-47 US-09-346-847-17 US-09-346-847-20 US-09-346-847-20 US-09-346-847-27 US-09-346-847-27 US-09-346-847-27 US-09-346-847-27 US-09-346-847-27 US-09-346-847-27 US-09-346-847-16 US-09-346-847-16 US-09-346-847-16 US-09-346-847-18 US-09-346-847-18 US-09-346-847-18 US-09-346-847-18 US-09-346-847-23 US-09-155-165-5 US-09-155-165-1 US-09-155-165-1 US-09-156-1448-3 US-09-466-772-1 US-09-466-772-1 US-09-466-772-1 US-09-466-772-1 US-09-466-772-1 US-09-466-772-1 US-09-466-772-1 US-09-466-772-1 US-09-466-772-1 US-09-162-524-1 US-09-162-524-1 US-09-162-524-1 US-09-163-34-1 US-09
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Sequence 7. Application US/08928958
Petent No. 5877282
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BLAKE, JAMES
APPLICANT: BLAKE, JAMES
APPLICANT: HAFFAR, OMAR K.
TITLE OF INVENTION: TRANSLOCATION HAVING NUCLEAR PROTEIN
TITLE OF INVENTION: TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND TITLE OF INVENTION: TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND TITLE OF INVENTION: MARGING OF USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 900 MIDDLEFIELD ROAD, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 92; DB 2; Length 16; 100.0%; Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EPOPPy disk
COMPUTER: Floppy disk
COMPUTER: Proppy disk
COMPUTER: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 5996-0019
FETERANION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5996-0019
TELEFAK: (650) 325-7812
TELEFAK: (650) 325-7823
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATTORNEY/SERISTICS:
LENGTH: 16 amino acids
TYPE: ATTORNEY/SERISTICS:
LENGTH: ATTORNEY/SERISTICS:
LENGTH: ATTORNEY/SERISTICS:
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ATTORNE
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AL IGNMENTS
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Best Local Similarity 100.0
Matches 16; Conservative
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MOLECULE TYPE: peptide
US-08-928-958-7
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USA
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STATE: CA
COUNTRY: USA
94025
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Gaps
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Patent No. 5920042
GENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Troy, Carol M.
TITLE OF INVENTION: DEATH AND USES THEREOF
TITLE OF INVENTION: DEATH AND USES THEREOF
TORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
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100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: RIOPSY disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR.1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELERENCE/DOCKET NUMBER: 0575/51247
TELERENCE/LOCKET NUMBER: 220.678
TELERENCE/LOCKET NUMBER: 220.678
TELERENCE/LOCKET NUMBER: 220.678
                                                                                                                                                           COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Pc_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: MARE: White Rsq., John P.
REDISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 0575/51247
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0526
INPORMATION FOR REQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FENDENCE CHARACTERISTICS:
FENDENCE CHARACTERISTICS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ROIKIWFONRRMKWKK 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-08-810-540-3
                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
          STREET: 1100
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                                                                                                USA
                                                                                                                        10036
                                                                     STATE: N
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GENERAL INFORMATION:
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Patent No. 5962415
GENERAL INFORMATION:
GENERAL FOR COMPRISING A PEPTIDE
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
TITLE OF INVENTION: IMMUNSUPPRESSANT AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                    Ouery Match

100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04 MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KIEIN, CIRISTOPHER: 34,363
REGISTRATION NUMBER: 34,363
REFERENCE/POCKET NUMBER: 000141b
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6, Application US/08964302A; Patent No. 6015787
; INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHRACTERISTICS:

LENGTH: 16 amino acids

; TYPE: amino acid

STRANDEDNESS: single

; TOPOLIGY: linear

; MULECULE TYPE: peptide

US-08-810-540-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMENTE (609) 252-57.
TELEPHONE (609) 252-4526
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
1.FNGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                          1 RQIKIWFQNRRMKWKK 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. Box 4(CITY: Princeton STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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US-08-964-302A-6
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US-09-072-429-7
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VENUAL 6
US.09-116-294-4

Sequence 4, Application US/09116294

Sequence 4, Application US/09116294

Patent No. 6025140

APPLICANT: Langel, Ulo

APPLICANT: Langel, Ulo

APPLICANT: Poogs, Margus

APPLICANT: Saar, Kulliki

APPLICANT: Andres

APPLICANT: Mathias

TITLE OF INVENTION: Conjugated Constructs of Peptides and

TITLE OF INVENTION: Conjugated Constructs of Peptides and

TITLE OF INVENTION: Moreler Acid Analogs, and Their Transport Across Membranes

FILE REFERENCE: 4394

CURRENT APPLICATION NUMBER: US/09/116,294

CURRENT APPLICATION NUMBER: 60/052,678

BARLIER FILING DATE: 1999-00-16

BARLIER FILING DATE: 1999-00-24

NUMBER OF SEQ ID NOS: 16

SOC ID NO 4

LENGTH: 16
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APPLICANT: Potter, David A.
APPLICANT: Skolnik, Paul R.
TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN
NUMBER OF SEQUENCES. IS
CORRESPONDENCE ADDRESS:
STREST: 225 Franklin Street
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                    CITY: bc.
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
ZOMPUTER: BADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPETE:
COMPUTER: TBM COMPETE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-964-302A-6
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3Y: linear
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Best Local Similarity
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ORGANISM: drosphila
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1 ROIKIWFONRRMKWKK 16
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-849-486-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-208-966-54
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US-08-849-486-4
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TITLE OF INVENTION: FOR THE INTRACELLULAR ADDRESSING OF ACTIVE MOLECULES
TITLE OF INVENTION: 10
COMPUTER READABLE FORM:
MEDLUM TYPE: Ploppy disk
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 Gaps
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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             COUNTY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MBDIUM TYPE: Diskette
COMPUTER: IEM COMPATIBLE
OPPERATING SYSTEM: Windows
SOFTWARE: FRALSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,614A
FILING DATE: 05-NOV-1997
CLASSIFICATION NUMBER: US/08/758,280
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/758,280
FILING DATE: 05-NOV-1996
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8535-0019-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08849486 Patent No. 6080724 GENERAL INFORMATION: APPLICANT:
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                                     1 ROIKIWFONRRMKWKK 16
                                                                   1 ROIKIWFONRRMKWKK 16
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                          USA
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US-08-849-486-1
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       Matches
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APPLICANT:
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                             GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
FILE REFERENCE: 48881/1742
CURRENT APPLICATION NUMBER: US/09/208,966
CURRENT APPLICATION NUMBER: US/09/208,966
CURRENT APPLICATION NUMBER: 60/082,402
EARLIER APPLICATION NUMBER: 60/069,012
EARLIER FILING DATE: 1998-04-20
EARLIER FILING DATE: 1997-12-10
MUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54
FLENTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Thangue, Nicholas B

APPLICANT: Bandara, Lasantha R

APPLICANT: Bandara, Lasantha R

ITILE OF INVENTION: Peptide antagonists of DP transcription factors

CURRENT APPLICATION NUMBER: US/09/308,935

CURRENT APPLICATION NUMBER: DCT/GB97/03506

EARLIER APPLICATION NUMBER: PCT/GB97/03506

EARLIER FILING DATE: 1997-12-22

EARLIER FILING DATE: 1996-12-20

MUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 16

"LENGTH: 16
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Pred. No. 2.1e-07;
Mismatches 0; Indels
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Patent No. 6294518
Patent No. 6294518
APPLICANT: Potter, David A.
APPLICANT: Skolnik, Paul R.
TITLE OF INVENTION: CALL-PERMEABLE PROTEIN INHIBITORS OF TITLE OF INVENTION: CALL-ABAIN
FILE REFERENCE: 00398-140001
CURRENT APPLICATION NUMBER: US/09/441,416A
Sequence 54, Application US/09208966
Patent No. 6221355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09308935
Patent No. 6268334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT / ORGANISM: Drosophila melanogaster US-09-308-935-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                              th 100.0%;
| Similarity 100.0%;
| 16; Conservative 0;
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Best Local Similarity
Matches 16; Conserv
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: human
US-09-208-966-54
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TITLE OF INVENTION: FOR TREATING BREAST CANCER
NUMBER OF SEQUENCES: 39
COMPOURER READABLE FORM:
MEDIUM IYPE: Floppy disk,
                                                                                                                                                                                                                                                                                                              .
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Sequence 33, Application US/09296089
Patent No. 6303576
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Byers, Stephen
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION
CURRENT FILING DATE: 1999-04-21
CURRENT FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTERO for Windows Version 3.0
                                                                                                                                                                                                                                                            Length 16;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/419,826
FILING DATE: 14-OCT-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/07711
                                                                                                                                                                                                                                                    Query Match
100.0%; Score 92; DB 3; Sest Local Similarity 100.0%; Pred. No. 2.1e-07; Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 92; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 08/964,302
PRIOR FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 6
LENGTH: 16
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FILING DATE: 14-APR-1998
APPLICATION NUMBER: US 60/043,545
FILING DATE: 14-APR-1997
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/09419826
Patent No. 6306832
GENERAL INFORMATION:
                                                                                                                                               TYPE: PRT
ORGANISM: Drosophila melanogaster
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LENGTH: 16
TYPE: PRT
ORGANISM: Drosophila melanogaster
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Gaps

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Best Local Similarity 100.0%; P:
Matches 16; Conservative 0;
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Sequence 10. Application US/09302305C

Sequence 10. Application US/09302305C

Sequence I.O. Application US/09302305C

Sequence I.O. Application Service

APPLICANT: Bernards, Rene

APPLICANT: Bernards, Rene

TITLE OF INVENTION: CC-Activators and Uses Thereof in Assays

TITLE OF INVENTION NUMBER: US/09/302,305C

CURRENT APPLICATION NUMBER: US/09/302,305C

PRIOR FILING DATE: 1999-04-30

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 10

LENGTH: 16

LENGTH: 16

LENGTH: 16
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1.0CATION: (1)...(16)
2.0CHEN INFORMATION: Translocation peptide derived from antennapedia
3.0THER INFORMATION: homeodomain protein
US-09-302-305C-10
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                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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US-09-346-847-1
Sequence 1, Application US/09346847
Sequence 1, Application US/09346847
Sequence 1, E472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
APPLICANT: Wang, Shudong
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCT-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 100.0
***rhes 16; Conservative
           16 amino acids
           LENGTH: 16 amino
TYPE: amino acid
STRANDEDNESS:
                                                                          linear
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US-09-419-826-35
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DB 4; Length 16;

100.0%; Score 92;

Query Match

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Sequence 47, Application US/09057363C
Sequence 47, Application US/09057363C
Patent No. 6551994
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
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NAME/KEY: MOD RES
LOCATION: LOCATION: AMIDATION
US-09-346-847-25
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STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OMPUTER: DEADLIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 08-APP-1998
CLASSIFICATION: «URKNOWN>
ATTORNEY AGENT INFORMATION:
COMPUTER TO THE TOPORMATION:
CLASSIFICATION: WINELE TO THE TOPORMATION:
REGISTRATION NUMBER: 44,614
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CORRESPONDENCE ADDRESS:
CORRESPONDENCES: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 92; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0;
Pred. No. 2.1e-07; 
; Mismatches 0;
                                                                                                                                                                                                                                          Sequence 25, Application US/09346847
Parent No. 6472507
GREERA INFORMATION:
APPLICANT: Fischer, M. Peter
APPLICANT: Fischer, M. Peter
APPLICANT: Wang, Shudong
TITLE OF INVENTION: Delivery System
TITLE OF INVENTION: Delivery System
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 16
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ORGANISM: Artificial Sequence
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US-09-346-847-25
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SEQ ID NO 29
LENGTH: 16
TYPE: PT:
ORGANISM: Artificial Sequence
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US-09-227-652B-4
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SEQ ID NO 4
LENGTH: 16
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APPLICANT: Rothbard, Jonathan B.
APPLICANT: Rothbard, Jonathan B.
APPLICANT: Rothbard, Paul A.
APPLICANT: McGrane, Paul A.
APPLICANT: McGrane, Paul A.
APPLICANT: Kirechberg, Thorsten A.
APPLICANT: Kirechberg, Thorsten A.
APPLICANT: Calldate, Inc.
ITILE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery;
ITILE OF INVENTION: Across and Into Epithelial Tissues
ITILE OF INVENTION: Across and Into Epithelial Tissues
CURRENT APPLICATION NUMBER: US 099/648,400A
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/150,510
PRIOR FILING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Lane, David P.
TITLE OF INVENTION: Cyclin Dependent Kinase Binding Compounds
FILE REFERENCE: CCI-003US
CURRENT APPLICATION NUMBER: US/09/043,560B
CURRENT APPLICATION NUMBER: 1999-04-07
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
LENGTH: 16
                                                                                                                                                                                                                                                                                                      Length 16;
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100.0%; Score 92; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0;
REFERENCE/DOCKET NUMBER: 100086.406
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: cunknown>
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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; Patent No. 6593292
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Patent No. 6569833
                                                                                                                                                                                                                                                                                                                                                                                                                               1 ROIKIWFONRRMKWKK 16
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ORGANISM: Artificial Sequence
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Best Local Similarity
---- 16; Conserva
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US-09-780-070-38

Sequence 38, Application US/09780070

Sequence 38, Application US/09780070

Sequence 38, Application US/09780070

Parent No. 663266

APPLICANT: Burke, James

APPLICANT: Burke, James

APPLICANT: Stritumter, Warren

APPLICANT: OF INVENTION: AND METHODS OF USE THEREOF

TITLE OF INVENTION: AND METHODS OF USE THEREOF

FILE REFERENCE: 5405.242

CURRENT FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/189,781

PRIOR APPLICATION NUMBER: 60/189,781

PRIOR PILING DATE: 2000-03-16

NUMBER OF SEQ ID NOS: 40

SOFTWARE PATENTING DATE: PATENTIN
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) OTHER INFORMATION: Description of Artificial Sequence:Penetratin 16-mer.
US-09-227-652B-4
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FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Antennapedia;

OTHER INFORMATION: homeodomain, Antennapedia-43-58
US-09-648-400A-29
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Patent No. 6610495
GENERAL INFORMATION:
APPLICANT TWW Telethon Institute for Child Health Research
TITLE OF INVENTION: PEPTIDE DETECTION METHOD
FILE REFERENCE: 199109/MRO. PCT
CURRENT APPLICATION NUMBER: US/09/227,652B
CURRENT FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: US 60/070989
PRIOR FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                  Score 92; DB 4; Length 16;
Pred. No. 2.1e-07;
Mismatches 0; Indels
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US-09-780-070-38
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                         1 ROIKIWFONRRMKWKK 16
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Best Local Similarity 100.
Matches 16; Conservative
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Search completed: October 1, 2004, 12:21:08 Job time : 19 secs
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54
LENGTH: 16
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                           Best Local Similarity
Matches 16; Conserv
                                                                                     ; TYPE: PRT
; ORGANISM: human
US-09-775-052A-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 22
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APPLICANT: Dowdy, Steven F.

TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF FILE REPERENCE: 48881/142

CURRENT APPLICATION NUMBER: US/09/775,052A

CURRENT FILING DATE: 2001-12-05

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/208,966

PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10

PRIOR FILING DATE: BARLIER FILING DATE: 1997-12-10

NUMBER OF SEQ ID NOS: 57
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                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURREALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/610,220B
FILING DATE: MAR-04-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 48332/JFW/JML
TELECOMMUNICATION NUMBER: 48332/JFW/JML
TELEFNOED POCKET NUMBER: 48332/JFW/JML
                   100.0%; Pred. No. 2.1e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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US-09-775-052A-54
Sequence 54, Application US/09775052A
Patent No. 6645501
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                                                                                                1 ROIKIWFONRRMKWKK 16
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                   Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / MOLECULE TYPE: peptide US-08-610-220B-9
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Best Local Similarity
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1 Sequence 2.2. Application US/09155165

1 Patent NO. 6660830

2 GENERAL INFORMATION:

APPLICANT: Radulascu, Razvan T

1 TILE OF INVENTION:

FILE REPERENCE: 201196/20

CURRENT FILING DATE: 1999-06-07

PRIOR PAPLICATION NUMBER: 09/155,165

PRIOR APPLICATION NUMBER: PC7/06943

PRIOR PILING DATE: 1999-09-22

PRIOR PILING DATE: 1998-09-22

PRIOR PILING DATE: 1996-03-26

PRIOR PILING DATE: 1996-12-20

PRIOR PILING DATE: 1996-12-20

PRIOR PILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 2.1
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COTHER INFORMATION: Description of Artificial Sequence: Peptide
NAMENTARY: PEPTIDE
LOCATION: (1) .. (16)
COTHER INFORMATION: Peptide
US-09-155-165-22
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Length 16;
                                                        Indels
100.0%; Score 92; DB 4; I
100.0%; Pred. No. 2.1e-07;
Live 0; Mismatches 0;
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October 1, 2004, 12:18:23 ; Search time 63.4 Seconds (without alignments) 81.211 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NBW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NBW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NBW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NBW_PUB.pep:*
7/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1351062 seqs, 321799191 residues
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 3,	Seguence	Sequence
SUMMARIES	US-08-610-220A-9 US-08-514-371-43	US-03-780-070-38	US-09-150-623-9	US-09-731-023A-10	US-09-854-204-1	US-09-900-147-8	US-09-792-480-29	US-09-785-802A-2	US-09-785-802A-5	US-09-902-432-32	US-09-953-031A-10	US-09-981-286A-3	US-09-962-967A-6	US-09-912-414-6
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Length DB	16	16	16	16	16	16	16	16	16	16	16	16	16	16
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Score	92	92	92	92	92	92	9	92	92	92	92	92	92	92
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Sequence 66, Appl
Sequence 15, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 75, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 63, Appl
                                                                                                                                                                                         Sequence 16, Appl
Sequence 18, Appl
                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08610220A
Publication No. US20030099638A1
GENERAL INFORMATION:
APPLICANT: TALE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 92; DB 8; Length 16; 100.0%; Pred. No. 3.1e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: DAEGHTIN Release #1.0, Version #1.30

SOFTWARE: PACENTIN Release #1.0, Version #1.30

SOFTWARE: NAX-04-1996

FILING DATE: NAX-04-1996

CLASSIFICATION NUMBER: US/08/610,220A

FILING DATE: NAX-04-1996

CLASSICATION: NAMBER: 28,678

REFERENCE/DOCKET NUMBER: 48332/JPW/JML

TELECOMMUNICATION INPORMATION:

MATERIAL OF AND PROPRATION:

NAME: White: John P.

REGISTRACION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 48332/JPW/JML
5 US-10-421-503-66
6 US-10-755-082-15
US-09-785-902A-14
6 US-10-364-645A-54
US-09-949-474-7
4 US-10-118-079-45
4 US-10-210-660-23
5 US-10-407-449-20
                                                                                                                                                   US-09-854-204-63
US-09-949-474-8
                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RQIKIWFQNRRMKWKK 16
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TELEPAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-09-214-371-43
US-09-214-371-43
Sequence 43, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David

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APPLICANT: Burke, James
APPLICANT: Burke, James
APPLICANT: Burke, James
APPLICANT: Strittmater, Warren
APPLICANT: Strittmater, Warren
APPLICANT: Strittmater, Warren
APPLICANT: Oxfoliate
TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT I
TITLE OF INVENTION: AND METHODS OF USE THEREOF
FILE REFERENCE: 5405.242
CURRENT APPLICATION NUMBER: US/09/780,070
CURRENT APPLICATION NUMBER: 60/189,781
PRIOR APPLICATION NUMBER: 60/189,781
PRIOR PLILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 40
SEQ THAN E: Patentin version 3.0
SEQ ID NO.38
LENGTH: 16
APPLICANT: Bottger, Angelica
APPLICANT: Chene, Parick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Freet, Pascal
APPLICANT: Freet, Pascal
APPLICANT: Freet, Pascal
APPLICANT: Freet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: 10509/214,371B
CURRENT FILING DATE: 1990-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
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; OTHER INFORMATION: Description of Artificial Sequence:peptide US-09-214-371-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09150623
; Patent No. US28020044931A1
GENERAL INFORMATION:
APPLICANT: Troy, Carol M
: TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
: NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 92; DB 9; Length 16; Best Local Similarity 100.0%; Pred. No. 3.1e-06; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 92; DB 9; Length 16; 100.0%; Pred. No. 3.1e-06; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/09780070; Patent No. US20020009752A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RQIKIWFQNRRMKWKK 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 43
LENGTH: 16
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1 ROIKIWFONRAKWKK 16

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TYPE: PRT
ORGANISM: Drosophila melanogaster
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Best Local Similarity 100.0%
Matches 16; Conservative
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US-09-900-147-8
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Patent No. US20020077283A1
GENERAL INFORMATION:
APPLICANT: Sessa, William
TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
FILE REFRENCE: 44574-5076-US
CURRENT APPLICATION NUMBER: US/09/731,023A
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/231,327
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
CUNTRY: U.S.A.
ZIP: 10036
COMPUTER: ELODRY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CUNRENT APDLICATION DATA:
APPLICATION NUMBER: US/09/150,623
FILING DATE: MAR-04-1996
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: 29,678
FILING DATE: MAR-04-1996
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REFERENCE/DOCKET NUMBER: 29,678
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0525
INFORMATION FOR ERO ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: DOMAIN
COTATION: (1)..(16)
COTHER INFORMATION: Homeodomain, internalization sequence
US-09-731-023A-10
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LENGTH: 16
TYPE: PRT
ORGANISM: Drosophila melanogaster
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Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-09-731-023A-10
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JOSEPHONE 8, Application US/0990147

JEACHT NO. US20020103121A1

JETLE OF INVENTION: Peptide antagonists of DP transcription factors

JITLE OF INVENTION: Peptide antagonists of DP transcription factors

JURENT APPLICATION NUMBER: US/09/900,147

CURRENT APPLICATION NUMBER: USALIER APPLICATION NUMBER: 09/308,935

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27

PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PATCHIN Ver. 2.1

LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 92; DB 9; I
100.0%; Pred. No. 3.1e-06;
tive 0; Mismatches 0;
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-900-147-8
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0; Indels

Query Match 100.0%; Score 92; DB 9; Length 16; Best Local Similarity 100.0%; Pred. No. 3.1e-06; Matches 16; Conservative 0; Mismatches 0; Indels

1 RQIKIWFQNRRMKWKK 16

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RESULT 11
US-09-902-432-32
; Sequence 32, Application US/09902432
; Pattent No. US20020160002A1
; GENERAL INFORMATION:
; APPLICANT: Itwin H. Gelman
; APPLICANT: Itwin H. Gelman
; APPLICANT: Susan G. Jaken
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A30559-A-FWC-A 070156.0597
; CURRENT PILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 08/978.277
; PRIOR APPLICATION NUMBER: 08/655,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR FILING DATE: 1996-06-18
; PRIOR FILING DATE: 1996-06-18
; RINGR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
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CTHER INFORMATION: Penetratin peptide
US-09-902-432-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Drosophila melanogaster
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1 ROIKIWFONRRMKWKK 16
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Best Local Similarity
Matches 16; Conserva
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GENERAL INFORMATION:
APPLICANT: Rothbard, Jonathan B.
APPLICANT: Wender, Paul A.
APPLICANT: Wender, Paul A.
APPLICANT: Xischberg, Thorsten A.
APPLICANT: Xischberg, Thorsten A.
APPLICANT: Xischberg, Thorsten A.
APPLICANT: Xischberg, Thorsten A.
APPLICANT: Calldate, Inc.
ITILE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
ITILE OF INVENTION: Across and Into Epithelial Tissues
ITILE OF INVENTION: Across and Into Epithelial Tissues
ITILE OF INVENTION: Across and Into Epithelial Tissues
GURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: US 60/150,510
PRIOR PLING DATE: 1999-08-24
SOFUTHOR PLING DATE: 1999-08-24
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; Sequence 2, Application US/09785802A
; Patent No. US20020151004A1
; Patent No. US2002015100A1
; APPLICANT: Craig, Roger
; TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
; TITLE REFERENCE: 11067/2035
; CURRENT APPLICATION NUMBER: US/09/785,802A
; PRIOR APLICATION NUMBER: US 09/748,06
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO
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US-09-785-802A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:Antennapedia OTHER INFORMATION: homeodomain, Antennapedia-43-58
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100.0%; Score 92; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ROIKIWFONRRMKWKK 16
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                                                              1 RQIKIWFQNRRMKWKK 16
                ROIKIWFONRRMKWKK 16
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US-09-792-480-29
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Sequence 5. Application US/09785802A

Sequence 5. Application US/09785802A

Fatent No. US20020151004A1

GENERAL INFORMATION:

APPLICATION: ROGER

TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME

TITLE OF INVENTION: DOI-1067/2035

CURRENT APPLICATION NUMBER: US/09/748,06

PRIOR PELICATION NUMBER: US 09/748,06

PRIOR PELICATION NUMBER: US 09/748,789

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 5.

LENGTH: 16
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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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Sequence 6, Application US/09912414

is Sequence 7, Application US/09912414

is publication No. US20030013169A1

is GENERAL INPORMATION:

is APPLICANT: Muller, Rolf

is APPLICANT: Montermann, Solva

is TITLE OF INVENTION: peptides and their use

is TITLE OF INVENTION: peptides and their use

is TITLE OF INVENTION: peptides and their use

is TITLE OF INVENTION: UNWERR: PCT/GB00/00227

is FRIOR APPLICATION NUMBER: PCT/GB00/00227

is PRIOR FILING DATE: 2000-01-26

is PRIOR FILING DATE: 1999-01-26

is NUMBER OF SEQ ID NOS: 40

is SEQ ID NO 6

is LENGTH: 16

is LENGTH: 16
APPLICANT: Potter, David A.

APPLICANT: Skolnik, Paul R.

TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN
FILE REPERENCE: 00398-14,006,962,967A

CURRENT APPLICATION NUMBER: US/09/962,967A

CURRENT APPLICATION NUMBER: US 09/441,416

PRIOR PILING DATE: 1999-11-16

PRIOR FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0

1 INNOTE: 0.
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Publication No. US20030054000A1
GENERAL INFORMATION:
APPLICANT Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF FILE REFERENCE: 48881/1742
CURRENT PELLING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: US/09/775,052
CURRENT FILING DATE: 1998-12-10
PRIOR FILING DATE: 1998-12-10
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100.0%; Score 92; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.1e-06;
trive 0; Mismatches 0;
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Drosophila melanogaster US-09-912-414-6
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Best Local Similarity 100.
Matches 16; Conservative
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US-09-775-052-54
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                                                                                                                     APPLICANT: Bernards, Rene
APPLICANT: Bernards, Rene
APPLICANT: Existen
APPLICANT: Existen, Renate
TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
TITLE OF INVENTION: Co-Activators and Uses Thereof in Assays
FILE REPERENCE: 4238/80713
CURRENT APPLICATION NUMBER: US/09/953,031A
PRIOR PELING DATE: 2001-12-05
PRIOR PELING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | NAME/KET: PEPTIDE | NAME/KET: PEPTIDE | LOCATION: (1)..(16) | OTHER INFORMATION: Translocation peptide derived from antennapedia | OTHER INFORMATION: homeodomain protein | US-09-953-031A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Publication No. US20020192799A1
GENERAL INFORMATION:
APPLICANT: Watowich, Stanley J.
APPLICANT: Waver, Scott C.
APPLICANT: Davey, Robert A.
ITLE OF INVENTION: Drug Discovery Methods
FILE REFERENCE: 265.0026010.
CURRENT APPLICATION NUMBER: US/09/981,286A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Cell-permeant polypeptide
US-09-981-286A-3
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PRIOR FLING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
                                                    Sequence 10, Application US/09953031A Patent No. US20020177177A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ROIKIWFONRRMKWKK 16
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Best Local Similarity 100.
Matches 16; Conservative
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16; Conservative
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US-09-981-286A-3
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LENGTH: 16
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, OTHER INFORMATION: Signal sequence peptide from Antennapedia homeodomain
US-09-933-780C-2
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| GENERAL INFORMATION:
| APPLICANT: Fahraeus, Robin
| APPLICANT: Lane, David P. |
| TITLE OF INVEWTION: Cyclin Dependent Kinase Binding Compounds TITLE OF INVEWTION: Cyclin Dependent Kinase Binding Compounds CURRENT FILING DATE: 2002-11-01
| PRIOR PAPLICATION NUMBER: US/10/286,964
| CURRENT PILING DATE: 1999-04-07 |
| NUMBER OF SEQ ID NOS: 16 |
| SEQ ID NO 3 |
| LENGTH: 16
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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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                    Length 16;
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              Query Match
100.0%; Score 92; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0;
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US-10-286-964-3
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Publication No. US20030096243A1
GENERAL INFORMATION:
Mulliam B
TITLE OF INVENTION:
Methods and Reagents for Live-cell Gene Expression Quantification
TITLE OF INVENTION:
Methods and Reagents for Live-cell Gene Expression Quantification
TITLE OF INVENTION:
METHOR PERIOR TOWNER: US/09/965,876A
CURRENT APPLICATION NUMBER: US 60/236,407
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
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US-09-295-189-4
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Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Woolf, Tod M.
TITLE OF INVENTION: Improved Antisense Oligomers
FILE REFERENCE: SRI-004
CURRENT APPLICATION UNMER: US/09/295,189 '
CURRENT FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
PRIOR APPLICATION NUMBER: 60/082,402
PRIOR FILING DATE: 1998-04-20
PRIOR APPLICATION NUMBER: 60/069,012
PRIOR FILING DATE: 1997-12-10
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54
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; OTHER INFORMATION: synthetic peptide US-09-965-876A-1
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ORGANISM: ARTIFICIAL SEQUENCE
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ORGANISM: Artificial Sequence
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Matches 16; Conserv
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ORGANISM: human
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YingNam Pan Chen
APPLICANT: Tingnin Michael Ramsey
APPLICANT: Michael Ramsey
APPLICANT: Michael Lloyd Sabio
TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
TITLE OF INVENTION: Inhibitors of the E2F-1/Cyclin
TITLE OF INVENTION: Inheraction for Cancer Therapy
FILE REFERENCE: 4-33243/P1/N1
CURRENT APPLICATION NUMBER: 2003-06-25
PRICR APPLICATION NUMBER: 10/024,935
PRICR APPLICATION NUMBER: PCT/FP1 /15006
PRICR APPLICATION NUMBER: PCT/FP1 /15006
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 16
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100.0%; Score 92; DB 12;
Best Local Similarity 100.0%; Pred, No. 3.1e-06;
Matches 16; Conservative 0; Mismatches 0;
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JOS-09-748-08-3.

PUBLICATION NO. US20010008758A1

GENERAL INFORMATION:

APPLICANT: MCHale, Anthony P.

APPLICANT: Craig, Roger

APPLICANT: Laro, Anna Maria Rollan

ITILE OF INVENTION: Delivery of an Agent

FILE REFERENCE: 11067/1060

CURRENT FILING DATE: 2000-012-22

PRIOR PILING DATE: 2000-07-24

PRIOR FILING DATE: 2000-07-24

PRIOR PILING DATE: 2000-07-30

PRIOR FILING DATE: 1999-07-33

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PARCHIN NOS: 3

SOFTWARE: PARCHIN NOS: 3

SOFTWARE: PARCHIN NOS: 3

LENGHIN: LARO NOS: 3

SOFTWARE: PARCHIN VERSION 3.1

SSOTUM NOS: 3
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                                                                                                                        RESULT 23
US-10-603-409-12
US-10-603-409-12
Sequence 12, Application US/10603409
Publication No. US20040053849A1
GENERAL INFORMATION:
1 ROIKIWFONRRMKWKK 16
                                    1 RQIKIWFQNRRMKWKK 16
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; ORGANISM: Drosophila sp.
US-09-748-063-3
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Best Local Similarity
Matches 16; Conserv
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US-09-748-063-3
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APPLICANT: Centre National
APPLICANT: Centre Nation
APPLICANT: Dupont, Edmond
APPLICANT: Dupont, Edmond
APPLICANT: Dupont, Edmond
APPLICANT: Prochiantz', Alain
TITLE OF INVENTION: Carrier vectors through an epithelium with tight junctions
TITLE OF INVENTION: Carrier vectors through an epithelium with tight junctions
FILE RÉPERBNES: 4563-506-103
CURRENT FILING DATE: 2003-05-20
FILOR APPLICATION NUMBER: PCT/FR01/03631
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: FR 00/14945
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 8
SSOFTWARE: PatentIn version 3.2
SSO ID NO 6
LENGTH: 16
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SEQUENCE 2, APPLICATION US. US20040054155A1

SEQUENCE INFORMATION:

APPLICANT: WOOLF, TOD M.

APPLICANT: TAYLOR, MARGARET F.

TILLE OF INVENTION: OLIGONUCLEOTIDE COMPOSITIONS WITH ENHANCED EFFICIENCY

FILE REFERENCE: 089586/0403

CURRENT APPLICATION NUMBER: US/1C/357,826A

CURRENT FILING DATE: 2002-02-03

PRIOR APPLICATION NUMBER: 60/353,381

PRIOR APPLICATION NUMBER: 60/353,203

PRIOR APPLICATION NUMBER: 60/436,236

PRIOR FILING DATE: 2002-02-01

PRIOR FILING DATE: 2002-12-13

PRIOR FILING DATE: 2003-10-7

NUMBER OF SEQ ID NOS: 58

SOSPWARE: Patentin Version 2.1

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Publication No. US20040029281A1
GENERAL INFORMATION:
                                                     1 RQIKIWFQNRRMKWKK 16
                ROIKIWFONRRMKWKK 16
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Matches 16; Conservative
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US-10-357-826A-2
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US-10-432-291-6
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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A; Molecule type: DNA A; Residues: 1-45 <OLI>
A; Accession: PC1216
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C;Species: Dugesia tigrina
C;Date: 30. Sep-1933 #sequence_revision 30. Sep-1993 #text_change 17-Oct-1997
C;Accession: PC1216
R;Oliver, G:; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlic
R;Oliver, G: Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlicher, G.; Vispo, M.; Ehrlicher, G.; M.; Shrite: Homeoboxes in flatworms.
A;Tritle: Homeoboxes in flatworms.
                                                                                                                                                                                                                                                                    antennapedia protein (clone pilos) - fruit fly (Drosophila pseudoobscura) (fragment) C;Species: Drosophila pseudoobscura C;Species: Drosophila pseudoobscura C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 15-Oct-1999 C;Accession: S57235 R;Randazzo, F.M.; Seeger M.A.; Huss, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C. Genetics 133, 319-330, 1993 A;File: Structural changes in the antennapedia complex of Drosophila pseudoobscura. A;Reference number: S57224
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Cispecies: Rattus norregious (Norway rat)
Cispecies: T-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999
Cispecies: T-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999
Cispecies: T-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999
Risakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.
Biochem. Genet. 32, 351-360, 1994
Airtie: Cloning of rat homeobox genes.
Airtie: Cloning of rat homeobox genes.
Airtie: Cloning of rat homeobox genes.
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C;Genetics:
A;Genetics:
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-42 <RES>
ALIGNMENTS
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A,Cross-references: FlyBase:FBgn0012693
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A; Residues: 1-33 <RAN>
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Cipate: 30-Sep-1931 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997

Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997

Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997

Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997

Ricession: Si5536

A; Title: Organization of human class I homeobox genes.

A; Reference number: Si536; WIID:90215256; PMID:2576652

A; Reference number: Si536; WIID:90215256; PMID:2576652

A; Reference number: Si536

A; Residues: lof compared with conceptual translation

A; Residues: lof cent.

Cigenetics:
A; Gene: GDB:HOXA

A; Cross-references: GDB:120647; OMIM:142950

A; Cross-references: GDB:120647; OMIM:142950

A; Reywords: DNA binding; homeobox; nucleus; transcription regulation

F; 2-S8/Domain: homeobox homology kHOX>
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Syleroy, P.; DeRobertis, E.M.

Dev. Dyn. 194, 21-32, 1992

A/Title: Effects of lithium chloride and retinoic acid on the expression of genes from the A; Reference number: IS1439; MUID:93043517; PMID:1384809

A; Accession: IS1439; MUID:93043517; PMID:1384809

A; Accession: IS1439; Ranslated from GB/EMBL/DDBJ

A; Residues: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-48 < LER>

A; Cross-references: GB:M91587; NID:9214257; PIDN:AAA49750.1; PID:9214258

C; Genetics:
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 15-Oct-1999
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A;Cross-references: EMBL:X66822
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-45/Domain: homeobox homology (fragment) <HOX>
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C.Superfamily: unassigned homeobox proteins; homeobox homology
C.Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-27/Domain: homeobox homology (fregment) <HOX>
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Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.9e-07;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                  Local Similarity 100.
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Best Local Similarity 100.0
Matches 16; Conservative
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R;Gaunt, S.J.; Coletta, P.L.; Pravtcheva, D.; Sharpe, P.T.
Development 109, 329-339, 1990
A;Title: Mouse Hox-3.4: homeobox sequence and embryonic expression patterns compared wit)
A;Reference number: A60084; MUID:90382249; PMID:1976088
A;Accession: A60084
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-71 cGAU>
C;Genetics:
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R;Fjose, A.; Molven, A.; Eiken, H.G.
Gene 62, 141-152, 1988
A;Title: Molecular cloning and characterization of homeobox-containing genes from Atlanti
A;Reference number: ISJ341, MUID:88226009; PMID:2897318
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R; Walldorf, U.; Fleig, R.; Gehring, W.J.
Rroc. Natl. Acad. Sci. US.A. 86, 9971-975, 1989
A; Title: Comparison of homeobox-containing genes of the honeybee and Drosophila.
A; Reference number: A34510; MUID:90099384; PMID:2574865
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C;Date: 22.Jun-1990 #sequence_revision 09-Oct-1992 #text_change 24-Sep-1999
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C;Species: Salmo salar (Atlantic salmon)
C;Date: i3-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
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A.Note: the authors mistranslated the codons for residues 68-74
C.Superfamily: unassigned homeobox proteins; homeobox homology
C.Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;9-65/Domain: homeobox homology <HOX>
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A/Residues: 1-75 <FJO>
A/Cross-references: GB-N18903; NID:g213797; PIDN:AAA49559.1; PID:g213798
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 15
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;5-61/Domain: homeobox homology <HOX>
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; Pred. No. 3e-07;
0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-74 <WAL>
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Domeotic protein Hox A6 - human (fragment)

N.Alternate names: homeotic protein Hox 1B

C;Becies: Home sapiens (man)
C;Becies: Homeosic protein Hox 1B

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997

C;Accession: S15538

R;Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc

A;Reference number: S15036; MUID: 90215256; PMID: 2576652

A;Accession: S1538

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JC1161
JC2161
JC2161
JC2161
JC2161
JC302
JC30
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C:Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999
C;Accession: A60084
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100.0%; Score 92; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 16; Conservative 0; Mismatches 0;
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homeotic protein Hox 3.4 - mouse (fragment)
                           ROIKIWFONRRMKWKK 16
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Best Local Similarity
Matches 16; Conserv
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A; Title: Molecular cloning and characterization of homeobox-containing genes from Atlant;
A; Reference number: 151341, MUID:88226009; PMID:2897318
A; Reference number: 151342
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-78 - FUO
A; Cross-references: GB:M18904; NID:g213799; PIDN:AAA49560.1; PID:g213800
C; Superfemally: unassistend homeobox proteins; homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F; 2-S8/Domain: homeobox homology < HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Denocic protein Hox-7 - Florida lancelet (fragment)
C;Species: Branchiostoma floridae (Florida lancelet)
C;Species: Branchiostoma floridae (Florida lancelet)
C;Date: 01-Feb-1995 #sequence_revision 26-May-1995 #text_change 24-Sep-1999
C;Accession: 847605
R;Garcia-Fernandez, 0.; Holland, P.W.H.
Nature 370, 563-566, 1994
A;Title: Archetypal organization of the amphioxus Hox gene cluster.
A;Reference number: 847509; MUID:94329179; PMID:7914353
A;Reference number: 847509; MUID:94329179; PMID:7914353
A;References: EMBL:235147; NID:9520617; PIDN:CAA84519.1; PID:9520618
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox, nucleus; transcription regulation
F;4-60/Domain: homeobox homology <HOX>
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Matches 16; Conservative
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Matches 16; Conservative
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Cidatession: 043559
Cidatessio
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C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
C;Accession: 151342
R;Fjose, A.; Molven, A.; Eiken, H.G.
Gene 62, 141-152, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 24-Sep-1999
C;Accession: C43559
                Gaps
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C,Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;20-76/Domain: homeobox homology (fragment) <HOX>
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100.0%; Score 92; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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           0; Indels
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100.0%; Pred. No. 3.2e-07;
tive 0; Mismatches 0;
           0; Mismatches
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                                                                                                                                                                        43 RQIKIWFQNRRMKWKK 58
                                                                                                          1 ROIKIWFONRRMKWKK 16
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Best Local Similarity 100.0
Matches 16; Conservative
           16; Conservative
           Matches
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homeotic protein Hox 2.2 precursor - mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Accession: B29585
R,Lonai, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.
DNA 6, 409-418, 1987
A;Fichai, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.
A;Fichai, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.
A;Fichain: Maw murine homeoboxes: structure, chromosomal assignment, and differential expresion: B29585
A;Feference number: A29585; MUID:88054465; PMID:2890503
A;Residuer type: DNA
A;Residuers: 1-81 clon.
A;Residues: 1-81 clon.
A;Residues: 1-81 clon.
A;Cross-references: GB:M18167
A;Note: the authors translated the codon CAG for residue 69 as Glu
C;Superfiamily: unassignad homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;4-60/Domain: homeobox homology <HOX>
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Score 92; DB 2; Length 81; Pred. No. 3.4e-07;
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Gaps

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C; Accession: A34510
R; Walldorf, U.; Fleig, R.; Gehring, W.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 9971-9975, 1989
A; Title: Comparison of homeobox-containing genes of the honeybee and Drosophila. A; Accession: A34510; WUID: 90099384; PMID: 2574865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homeotic protein H55 - honeybee (fragment)
C;Species: Apis mellifera (honeybee)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 24-Sep-1999
           A; Cross-references: EMBL: Z35145; NID: 9520613; PIDN: CAA84517.1; PID: 9520614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <WAL>
A;Residues: 1-86 <WAL>
A;Cross-references: GB:M29488; NID:g155665; PIDN:AAA27723.1; PID:g155666
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;9-65/Domain: homeobox homology <HOX>
                                                  C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;7-63/Domain: homeobox homology <HOX>
                                                                                                                                                                                                 Score 92; DB 2; Length 83;
Pred. No. 3.4e-07;
/ Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 16; Conservative 0;
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Best Local Similarity 100.0
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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847603
howeolic protein Hox-5 - Florida lancelet (fragment)
C;Species: Branchiostoma floridae (Florida lancelet)
C;Species: Branchiostoma floridae (Florida lancelet)
C;Species: Branchiostoma floridae (Florida lancelet)
C;Accession: 847603
R;Garcia-Fernandez, U.; Holland, P.W.H.
Nature 370, 563-566, 1994
A;Title: Archetypal organization of the amphioxus Hox gene cluster.
A;Reference number: 847599; MUID:94329179; PMID:7914353
A;Accession: 847603
A;Status: preliminary
A;Molecule type: DNA
A;Residuae: 1-83 cGAR.
A;Residuae: 1-83 cGAR.
A;Cross-references: EMBL:235145
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;7-63/Domain: homeobox homology <HOX>
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ROIKIWFONRRMKWKK
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Best Local Similarity 100.0
Matches 16; Conservative
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Matches 16, Conservative
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      Length 86;
100.0%; Score 92; DB 2; I 100.0%; Pred. No. 3.6e-07; cive 0; Mismatches 0;
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1 RQIKIWFQNRRMKWKK 16
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homeotic protein MM3 - African clawed frog (fragment)
homeotic protein MM3 - African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30.5ep-1993 #sequence_revision 30.5ep-1993 #text_change 24-Sep-1999
C;Date: 30.5ep-1993 #sequence_revision 30.5ep-1993 #text_change 24-Sep-1999
C;Accession: A03317
R;Muller, M.M.; Carrasco, A.E.; DeRobertis, E.M.
Cell 39, 157-162, 1984
A;Title: A homeo-box-containing gene expressed during oogenesis in Xenopus.
A;Reference number: A03317; MUID:85024889; PMID:6207937
A;Reference number: A03317, MUID:85024889; PMID:6207937
A;Molecule type: DNA
A;Residues: 1.88 cMUL>
A;Molecule type: DNA
A;Residues: 1.68 cMUL>
A;Generics:
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S00589

homeotic protein Hox 5 - African clawed frog (fragment)

homeotic protein Hox 5 - African clawed frog)

homeotic protein Hox 5 - African clawed frog)

homeotic protein Hox 5 - African clawed frog)

c) bate: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 24-Sep-1999

C) Accession: S00589

MITIELS And Res. 16, 1453-1469, 1988

A; Reference number: S00589; MUID:88157707; PMID:2894634

A; Reference number: S00589; MUID:88157707; PMID:2894634

A; Residues: 1-87 < FRIA

A; Coss-references: EMBL:X07105; NID:g64757; PIDN:CAA30126.1; PID:e12307; PID:g1334653

A; Cross-references: EMBL:X07105; NID:g64757; PIDN:CAA30126.1; PID:e12407; PID:g1334653

C; Superfamily: unassigned homeobox, nucleus; transcription regulation

F; 21-77/Domain: homeobox homology < HOX>
C;Species: Gallus gallus (chicken)
C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
C;Accession: S08303
B;Wedden, S.E.; Pang, K.; Eichele, G.
Development 105, 639-650, 1989
A;Title: Expression pattern of homeobox-containing genes during chick embryogenesis.
A;Reference number: S08302; MUID:90126373; PMID:2575515
A;Accession: S08303
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 < WED>
A;Residues: 1-86 < WED>
A;Cross-references: EMBL:X16847
C;Superfamily: unassigned homeobox, nucleus; thanscription regulation
F;10-66/Domain: homeobox homology <HOX>
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100.0%; Pred. No. 3.6e-07;
.ive 0; Mismatches 0; Indels
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Matches 16; Conservative
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homeotic protein Hox B6 - human (fragment)

NyAlternate names: homeotic protein Hox 2B; homeotic protein Hu2
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: homeotic protein Hox 2B; homeotic protein Hu2
C;Species: Homo sapiens (man)
C;Accession: A05266; 31537

S;Levine, M.; Rubin, G.M.; Tjian, R.
Cell 39, 667-673, 1984
A;Title: Human DNA sequences homologous to a protein coding region conserved between home
A;Title: Human DNA sequences homologous to a protein coding region conserved between home
A;Title: Human DNA sequences homologous to a protein coding region conserved between home
A;Title: Human DNA sequences homologous to a protein coding region conserved between home
A;Title: Human DNA sequences homologous to a protein coding region conserved between home
A;Title: Type: DNA
A;Residues: 196 cLEV>
A;Note: this reading frame extends between two stop codons and does not begin with a stan
A;Note: this reading frame class I homeobox genes.
A;Note: this reading frame class I homeobox genes.
A;Note conman and class I homeobox genes.
A;Reference number: S18036; MUID: 90215256; PMID: 2576652
A;Notession: S1537
A;Note: DNA
A;Residues: 18-19, K', 21-83 <BON>
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A;Gene: GDB:120659; OMIM:142961
A;Cross-references: GDB:120659; OMIM:142961
A;Map position: 17g21.3-17g21.3
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;19-75/Domain: homeobox homology <HOX>
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October 1, 2004, 12:04:01; Search time 8.8 Seconds (without alignments) 94.673 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scription	P31256 xenopus lae Q28599 ovis aries Q28659 ovis aries P31262 notophthalm P15860 opis mellif P0656 salmo salar P1886 rattus norry P09637 salmo salar P81192 lineus sang P09013 brachydanio P14838 gallus gall P15859 apis mellif P009020 xenopus lae P009018 brachydanio P15859 apis mellif P15859 apis mellif P15859 apis mellif P009020 xenopus lae P009018 trattus norv P25274 brachydanio P18864 rattus norv P25208 ambystoma m P49925 ovis aries Q31171 xenopus lae Q90171 xenopus lae Q90171 xenopus lae P04476 kenopus lae P04476 kenopus lae P09629 homo sapien P32043 mus musculu P17509 homo sapien P09023 mus musculu P17509 homo sapien P09023 mus musculu P17509 homo sapien
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Wararyota, Metazoca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinee; Ovis.
                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
PROSITE; PS0011; HOMEOBOX 2; 1.
PROSITE; PS05011; HOMEOBOX 2; 1.
Transcription regulation.
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 92; DB 1; Length 48; 100.0%; Pred. No. 2.5e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 AA; 5716 MW; BC39E36822EDDD2A CRC64;
                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOXB6 OR XIHOX-2.2; (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
HOMAS OR HOXA-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMEOBOX
                                                                          Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                  EMBL, M91587, AAA49750.1; -.
PIR, 151439, 151439.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox. 1.
                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 ROIKIWFONRRMKWKK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                       Xenopodinae; Xenopus.
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=8355;
        HXB6 XENLA
P31256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HXAS SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
DNA BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HXAS SHEEP
HXB6_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                 0; Gaps
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-!- FUNCTION: Sequence-specific transcription factor which is part a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-!- SUBCELLUMAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep).
Bakaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00024; HOMEOBOX.

Prodon; PR000010; Homeobox; 1.

PROSITE; PS00027; HOMEOBOX_1; 1.

PROSITE; PS0017; HOMEOBOX_1; 1.

PROSITE; PS0017; HOMEOBOX_2; 1.

Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 92, DB 1; Length 49; 100.0%; Pred. No. 2.5e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 AA; 6331 MW; 1EE702315E7C099B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-PSB-2003 [Rel. 41, Last annotation update)
HOMEODOX PICTEIN HOX-A7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMEOBOX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001356; Homeobox. Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U61978; AAB04754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RQIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 ROIKIWFONRRMKWKK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
tes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P02833; 1HOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                              SEQUENCE FROM N.A.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
DNA BIND
NON TER
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ID HXA7_SHB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=9220273; PubMed=1351019;
Belleville S., Beauchemin M., Tremblay M., Noiseux N., Savard P.;
"Homeobox-containing genes in the newt are organized in clusters similar to other vertebrates.";
Gene 114:179-186(1992).
-!-FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-!-SUBCELLULAR LOCATION: Nuclear.
-!-SUBLERLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
Homeobox protein Hox-C5 (NvHbox-3.4) (Fragment).
Notophthalmus viridescens (Zastern newt) (Triturus viridescens).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Naphibia; Batrachia, Caudata, Salamandroidea, Salamandridae;
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                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0024; HONEDSOX.
PRINTS; PRO0011; HTHREPRESR.
ProDom; PD000101; Homeobox; 1.
ProSITE; PS00127; HOMEOBOX; 1.
PROSITE; PS0017; HOMEOBOX 1; 1.
PROSITE; PS0017; HOMEOBOX 2; 1.
TROSITE; PS0017; HOMEOBOX 2; 1.
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 92; DB 1; Length 71; 100.0%; Pred. No. 3.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 AA; 8888 MW; 931049FAC1BAACB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                       InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH lambrepressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M84001; AAA49397.1; ALT_INIT.
PIR; JC1161; JC1161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P02833; 1SAN.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                            EMBL; U61979; AAB04755.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RQIKIWFQNRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 ROIKIWFONRRMKWKK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00024; HOMEOBOX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                             Pfam; PF00046; homeobox;
                                                                                                                                                                                               HSSP; P02833; 9ANT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HXC5_NOTVI
ID HXC5_NOTVI
AC P31262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
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BIND
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                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R HSSF; P02833, 1HOM.

R InterPro; 1PR001356; Homeobox.

R Pfam; P000046; Homeobox; 1.

R PRINTS; PR00024; HOMEOBOX.

R Prolom; P0000100; Homeobox; 1.

R PROSITE; PS00027; HOMEOBOX.

R PROSITE; PS00027; HOMEOBOX.

R PROSITE; PS00011; HOMEOBOX.

R PROSITE; PS00011; HOMEOBOX.

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I SEQUENCE 74 AA; 9263 MW; 5FCBFB4F723D3837 CRC64;
                SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMBODOX; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 92; DB 1; Length 74; Best Local Similarity 100.0%; Pred. No. 4e-08; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                         Length 71;
                                                                                                                                                                                                      100.0%; Score 92; DB 1; Length 71
100.0%; Pred. No. 3.9e-08;
Live 0; Mismatches 0; Indels
                                                                                                                                                                      71 AA; 8979 MW; 07999FDE89995B42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila.";
Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
-: SUBCELLUAR LOCATION: Nuclear (Potential).
-: SIMILARITY: Belongs to the Antp homeobox family.
-: SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Homeobox protein H90 (Fragment)
Apis mellifera (Honeybee).
                                                                                                                                       HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                            1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                            46 ROIKIWPONRRMKWKK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M29493; AAA27728.1; -.
                                                                                                                                                                                                                      Local Similarity 100.0 tes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; D34510; D34510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apidae, Apis
                                                                                                                                                                                                                                                                                                                                                                                             HM90 APIME
P15860;
                                                                                                                      NON TER
DNA BIND
NON TER
SEQUENCE
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                              RESULT 5
HM90_APIME
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us-09-830-779-7.rsp

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                                                                                                                                                                                      Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                            STRAIN=Sprague-Dawley, BubMed=2907739, MacDinEs=85231502, PubMed=2907739, Palzon M., Chung S.Y., BubMed="The expression of rat homeobox-containing genes is developmentally "The expression of rat homeobox-containing genes is developmentally and the expression of rat homeobox-containing genes is developmentally and the expression of rat homeobox-containing genes is developmentally and the expression of rat homeobox-containing genes is developmentally and the expression of rat homeobox.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae; Salmo.
NCBI TaxID=8010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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PRINTS; PRODUCT4; HOMEOBOX; 1.
PRINTS; PRODUCT4; HOMEOBOX.
PRODUCT5; PRODUCT5; HOMEOBOX.
PRODUCT5; PRODUCT5; HOMEOBOX.
PROSTITE; PRODUCT7; HOMEOBOX.
PROSTITE; PRODUCT7; HOMEOBOX.
PROSTITE; PROSTITE; PROMEOBOX.
PROMEOBOX: DNA-binding; Developmental protein; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 92; DB 1; Length 76; 100.0%; Pred. No. 4.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMEOBOX.
5235F665C0672385 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-AAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-A5 (S12-B) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P02833; 9ANT.
InterPro; IPR01827; Antennapedia.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_lambrepressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=88226009; PubMed=2897318;
Fjose A., Molven A., Elken H.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M37567; AAA41343.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RQIKIWFQNRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 AA; 9293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 ROIKIWFONRRMKWKK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; C43559; C43559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                        SEQUENCE FROM N.A.
                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                        subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALSA
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DNA BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HXA5_SALSA
ID HXA5_SALSAC P09637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fjose A., Molven A., Eiken H.G., "Molecular cloning and characterization of homeo-box-containing genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
10-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 12, Last amoctation update)
Homeobox protein S12-4 (Fragment).
Salmo salar (Atlantic salmon).
Actinopterygii; Necoterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homeobox; DNA-binding; Developmental protein; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 92; DB 1; Length 75; 100.0%; Pred. No. 4.1e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 AA; 9330 MW; FC02C3672F35475D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
HOMEODOX protein Hox-C4 (R3) (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMEOBOX.
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
MEDLINE=88226009; PubMed=2897318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PRODOZ4; HOMEOBOX.
Prodom; PD00010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, M18903; AAA49559.1; -.
PIR, I51341; I51341.
HSSP, P02833; 9ANT
INCEPPO; IPR001356; Homeobox.
  1 RQIKIWFQNRRMKWKK 16
                                              50 ROIKIWFONRRMKWKK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RQIKIWFQNRRMKWKK 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Atlantic salmon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
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SEQUENCE
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P18865;
                                                                                                                                        HMSA_SALSA
                                                                                                                                                                                            SOUTH THE SOUTH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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Gaps

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RESULT 10
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0
                            from Atlantic salmon.";

Gene 65:141-152(1988).

-!- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.

-!- SUBCELLUTAR LOCATION: Nuclear.

-!- SIMILARITY: Belongs to the Antp homeobox family.
"Molecular cloning and characterization of homeo-box-containing genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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PRINTS; PRO0024; HOWEDOX; 1.
SMART; SM00039; HOMEODOX; 1.
PROSITE; PS000027; HOMEODOX 1; 1.
PROSITE; PS000027; ANTENNAPEDIA; PARTIAL.
PROSITE; PS000011; HOMEOBOX 2; 1.
HOMEODOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lineus sanguineus (Ribbon worm).
Bukaryota, Metazoa, Nemertea, Anopla, Heteronemertea, Lineidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULÂR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 92; DB 1; Length 78; 100.0%; Pred. No. 4.3e-08; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 60 HOMEOBOX.
78 AA; 9489 MW; 828DEBDDF78AC820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Homeobox protein Hox-A4 (LsHox 4) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 AA
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InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001827; Antennapedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M18904; AAA49560.1; -. PIR; I51342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RQIKIWFQNRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 ROIKIWFONRRMKWKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
16s 16; Conservative
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HXA4 LINSA
AC P81192;
DT 15-JUL-1998
DE HOMEODOX Prol
GN Lineus.
OX Lineus.
OX NCBI TAXID=41
RN (1)
RN REDLINE=9816;
RR Kmita-Cuniss
RR Kmita-Cuniss
RR Kmita-Cuniss
RT implications
RL Proc. Natl.;
CC -1- FUNCTION
CC Specific
CC -1- SIMILARI:
CC -1- SI
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DNA BIND
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                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOXBES OR ZFS4 OR ZF-54.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii; Teleostei, Ostariophysi, Cypriniformes,
NCBI_TaxID=7955;
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0
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Transcription regulation.
                                                                                                                                                                                                                         100.0%; Score 92; DB 1; Length 80; 100.0%; Pred. No. 4.4e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P02833; 1SAN.
ZFIN; ZDB-GENE-000823-6; hoxb5b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                          1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                   53 ROIKIWFONRRMKWKK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X12803; CAA31291.1; -.
                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.'
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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us-09-830-779-7.rsp

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49 ROIKIWFONRRMKWKK 64
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                                                                HXB6 CH1 P14839;
                                                 CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                           Development 105:639-650(1989).

-!- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-!- SUBCELLULAR LOCATION Nuclear.
-!- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                                                                                                                                                    HOXBS OR GHOX-2.1.
Gallus gallus (Chicken).
Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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0
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PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00032; ANTENNAPEDTA; PARTIAL.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                TISSUE=Erythrocyte;
MEDLINE=90126373; PubMed=2575515;
Wedden S.E., Pang K., Eichele G.;
Expression partern of homeobox-containing genes during chick embryogenesis.";
                                               / Match 100.0%; Score 92; DB 1; Length 81; Local Similarity 100.0%; Pred. No. 4.4e-08; les 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 92; DB 1; Length 82; 100.0%; Pred. No. 4.5e-08; Live 0; Mismatches 0; Indels
 1 1 6 65 HOMEOBOX.
81 AA, 9977 MW, B7698AEFFEB3C6B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 66 HOMEOBOX.
82 AA; 9877 MW; 53F70ACDC9FDEF8F CRC64;
                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
HOXB5 OR GHOX-2.1) (Fragment)
                                                                                                                                                                                        82 AA
                                                                                                                                                                                        STANDARD; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P02833; ISAN.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X16846; CAA34743.1; -. PIR; S08302; S08302.
                                                                                                   1 ROIKIWFONRRMKWKK 16
                                                                                                                            48 ROIKIWFONRRMKWKK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                      HXB5_CHICK
P14838;
NON TER
DNA BIND
SEQÜENCE
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DNA_BIND
SEQUENCE
                                                   Query Match
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                                                                                                                                                                            HXB5_CHICK
                                                                           Matches
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1 ROIKIWFONRRMKWKK 16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embryogeneals.";
Development 105:639-650(1989).
-- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides calls with specific positional identities on the anterior-posterior axis.
--- SUBCELDUAR LOCATION: Nuclear.
--- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00032; ANTENNAPĒDIA; PARTIAL.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Devēlopmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Erythrocyte;
MEDLINE=90126373; bubMed=2575515;
Wedden. S.L., Pang K., Eichele G.;
"Expression pattern of homeobox-containing genes during chick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 92; DB 1; Length 84; 100.0%; Pred. No. 4.6e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMEOBOX.
BC06B10165B19E71 CRC64;
                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOMEODA protein HOA-B6 (GHOX-2.2) (Fragment)
HOXB6 OR GHOX-2.2
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AA.
84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X16847, CAA34744.1; -...
PIR, S08303, S08303.
HSSP, P02833, 1H0M.
InterPro, IPR001827, Antennapedia.
InterPro, IPR001356, Homeobox.
InterPro, IPR00147, HTH_lambrepressr.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 AA; 10279 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RQIKIWFQNRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 ROIKIWFONRRMKWKK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 16; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00046; homeobox
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
SCR APIME
ID SCR APIME
AC P15859;
CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
DNA BIND
SEQUENCE
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NCBI_TaxID=9823;
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SEQUENCE
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P09078;
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                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
-!- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-!- SUBCELLUAR LOCATION: Nuclear.
-!- SUBCELLUAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY. STRONGEST, TO SCR OF DROSOPHILM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craníata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homeobox; DNA-binding; Developmental protein; Nuclear protein.
                                                                                                                    MEDLINE=90099384; PubMed=2574865; Walldorf U., Fleig R., Gehring W.J.; "Comparison of homeobox-containing genes of the honeybee and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 92; DB 1; Length 86; 100.0%; Pred. No. 4.7e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 AA; 10713 MW; 2A49AB857C138AB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
HOMEODA POCTEIN HOX-C5 (XIHDOX-5) (Fragment).
HOXC5 OR XLHBOX5.
01-APR-1990 (Rel. 14, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
Amecbox protein H55 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00032; ANTENNAPEDIA; PARTIAL. PROSITE; PS00027; HOMEOBOX 1; 1. PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                       HSSP; PO2833; ISAN.
InterPro; PR001827; Antennapedia.
InterPro; IPR001856; Homeobox.
Pfam; PF00046; homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                 EMBL; M29488; AAA27723.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 ROIKIWFONRRMKWKK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
1es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                             PIR; A34510; A34510.
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                  NCBI TaxID=7460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
                                                                                                                                                         Drosophila.";
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P09020;
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NON_TER
SEQUENCE
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Matches
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 RXX OOC OOR DETAIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *************************
MEDLINE=88157707; PubMed=2894634;
Fritz A., de Robertis E.M.;
"Xenopus homeobox-containing CDNAs expressed in early development.";
"Nucleic Acids Res. 16:1453-1469 (1988).
-!- FUNCTION: Sequence-specific transcription factor which is part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 16:10364-10364(1988).

-!- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.

-!- SUBCELLUMAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDINES-2904133; MEDINES-89057478; PubMed=2904133; MAILLE J.R., Gaunt S.J., Sharpe P.T.; "Pig Hox-2.4 has accumulated a frameshift mutation relative to mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                 a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-:- SUBCELLULAR LOCATION, Nuclear.
-:- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN EARLY EMBRYOS.
-:- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R BMB1, X07105; CAA30126.1; -
R PIR; S00589; S00589.
R HSSP; P02683; 94MT.
R TRANSFAC; T03765; -
R InterPro; IPR001836; Hameobox.
R InterPro; IPR001836; Homeobox.
R FRINTS; PR00046; Homeobox.
R PRINTS; PR00046; HOMEOBOX.
R PRINTS; PR000401; HOMEOBOX.
R PATINTS; PR00024; HOMEOBOX.
R PATINTS; PR00024; HOMEOBOX.
R PATINTS; PR00027; HOMEOBOX.
R SWART; SM00389; HOX; I.
R PROSITE; PS00027; HOMEOBOX 1; 1.
R PROSITE; PS00027; ANTENNAPEDIA; 1.
R PROSITE; PS00027; ANTENNAPEDIA; 1.
R PROSITE; PS00011; HOMEOBOX 2; 1.
M Homeobox; DNN-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 92; DB 1; Length 87
100.0%; Pred. No. 4.8e-08;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 10 ANTP-TYPE HEXAPEPTIDE.
20 79 HOMEOBOX.
87 AA; 11058 MW; E67939E334E2BA43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
26-FBE-2003 (Rel. 41, Last annotation update)
HOMECDOX protein Hox-B8 (Hox-2.4) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Query Match
Best Local Similarity 100.000
Best Local Similarity
16; Conservative
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SMART; SM00389; HOX; 1.
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DNA BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                     RESULT 17
HXA7_RAT
ID HXA7_RAT
AC P09634;
                                                                                                                                                                                                                                Query Match
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the SAISS Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license discent (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, Last annotation update)
190XC6 OR HOXC6A OR (ZF-61) (Fragment).
190XC6 OR HOXC6A OR HOX-C6 (DR ZF-61)
190XC6 OR HOXC6A OR GEDSAGISH) (Danio rerio).
190XC4ATYOCTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Nibi_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                     Pfam; PF00146; homeobox; 1.

PRINTS; PR0024; HOMEOBOX.

PRINTS; PR00031; HTHREPRESSR.

SMART; SM00389; HOX; 1.

SMART; SM00389; HOX; 1.

PROSITE; PS000021; ANTENNAPEDIA; PARTIAL.

PROSITE; PS50017; HOMEOBOX 1; 1.

PROSITE; PS50011; HOMEOBOX 2; 1.

Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                     100.0%; Score 92; DB 1; Length 93; 100.0%; Pred. No. 5.1e-08; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               7841DD6D17634EEC CRC64;
-!- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                     InterPro, IPR001827, Antennapedia.
InterPro, IPR001356, Homeobox.
InterPro, IPR000047, HTH_lambrepressr.
                                                                                                                                                                                                                                                                                                     HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                               EMBL; X06668; CAB57825.1; ALT_SEQ.
HSSP; P02834; 1B81.
                                                                                                                                                                                                                                                                                                               93 AA; 10872 MW;
                                                                                                                                                                                                                                                                                                                                                                                     1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                         49 ROIKIWFONRRMKWKK 64
                                                                                                                                                                                                                                                                              ranscription regulation.
                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
1es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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P15862;
                                                                                                                                                                                                                                                                                         NON TER
DNA BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                              Matches
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-!- SUBCELLUTAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley,
MEDLINE=87277429; PubMed=2886401;
Falzon M., Sanderson N., Chung S.Y.;
"Cloning and expression of rat homeo-box-containing sequences.";
Gene 54:23-32(1987).
                                                                                                                                                                                            PERMY: PF00046; homeobox; 1.

PRINTS; PR00024; HOMEOBOX.

PRODOUT PN000010; Homeobox; 1.

PROSITE; SN00389; HOX; 1.

PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS00011; HOMEOBOX 2; 1.

PROSITE; PS00011; HOMEOBOX 2; 1.

Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 92; DB 1; Length 96; 100.0%; Pred. No. 5.3e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 AA; 11638 MW; FIED7AFAA3B640C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
88-FBB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-A7 (Hox-1.1) (R5) (Fragment).
HOXA7 OR HOXA-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M16807; -; NOT ANNOTATED CDS. PIR; A27471; A27471. HSSP; P02833; 9ANT. TATANSFA; T01707; -. InterPro; IPR001827; Antennapedia. InterPro; IPR001356; Homeobox.
                                                                 HSSP; PO2833; 9ANT.
ZFIN; ZDB-GRNE-990415-113; hoxc6a.
InterPro; IPR001827; Anternapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ROIKIWFONRRMKWKK 16
EMBL; X17266; CAA35170.1; -. PIR; S08639; S08639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 ROIKIWPONRRMKWKK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.

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Fri Oct 1 16:13:12 2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prince V.E., Moens C.B., Kimmel C.B., Ho R.K.;

Prince V.E., Moens C.B., Kimmel C.B., Ho R.K.;

"Zebrafish hox genes: expression in the hindbarin region of wild-type and mutants of the segmentation gene, valentino.";

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-! SUBCELLUIAR LOCATION: Nuclear.
-! SUMILARITY: Belongs to the Antp homeobox family. Deformed
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 38, Last annotation update)
HOMBOOX protein Hox-B4 (ZF-13) (Fragment).
HOXB4 OR HOXB4A OR HOX-B4 (ZF-13) (Fragment).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygui, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCB1_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89211958; PubMed=2468579;
Njoelstad P.R., Molven A., Eiken H.G., Fjose A.;
"Structure and neural expression of a zebrafish homeobox sequence.";
                                                                                                                                                                                                           .
0
100.0%; Score 92; DB 1; Length 105; 100.0%; Pred. No. 5.9e-08;
                                                                                                                                                                                                        0; Indels
                                                                                                      HOMEOBOX.
GLU-RICH (ACIDIC).
; 106C1DF938F2864B CRC64;
                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M24085; AAAS6866.1; ALT_INIT.
EMBL; Y13946; CAA74284.1; -.
TIR; JT0489; JT0489.
HSSP; P02833; 9ANT.
ZFIN; ZDB-GENE-990415-105; hoxb4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001827; Antennapedia.
InterPro, IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                       DOMĀIN 91 105 GI
SEQUENCE 105 AA; 12552 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                            1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                            47 ROIKIWFONRRMKWKK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-86 FROM N.A.
                                                                                                                                                                                                          16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 73:33-46(1988).
                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                              HXB4_BRARE
ID HXB4_BRARE ST
AC P22574; 042369;
DT 01-AUG-1991 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulated and tissue specific.";
Development 103:601-610(1988).
-!- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-!- SUBCELULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Predominantly spinal cord and kidney.
-!- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley,

BEDLINE-S9311502, PubMed=2907739,

FAIZON M., Chung S.Y., Chung S.Y.,

"The expression of rat homeobox-containing genes is developmentally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P02833; 9ANT.
InterPro; IPR001825; Antennapedia.
InterPro; IPR001856; Homeobox.
Pfam; PP00046; homeobox;
PRINTS; PR00041; HOMEOBOX.
PRINTS; PR000401; Homeobox; 1.
PROSTTE; PS00032; ANTENNAPEDIA; PARTIAL.
PROSTTE; PS0027; HOMEOBOX 1; 1.
PROSTTE; PS0027; HOMEOBOX 2; 1.
PROGEOPOX; DNA-Dinding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
                                                                                                                                                                                              Length 105;
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                                                                                                                                                        Score 92; DB 1; Lengtn Luz
Pred. No. 5.9e-08;
                                                                                          10 69 HOMEOBOX.
105 AA; 12262 MW; BOEFD84D909289F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AA; 13910 MW; 099B6F064DC47C28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-F82-2003 (Rel. 41, Last annotation update)
HOMEOBOX protein Hox-B7 (R1B) (Fragment).
                                                                                                                                                           100.0%; Scc...
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 112 AA.
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                                                                                                                                                                                                                                                                                                                       1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                 52 ROIKIWFONRRMKWKK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M37566; AAA41342.2; -.
                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                              NON TER
DNA BIND
SEQUENCE
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DNA BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HXB7 RAT P18864;
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HXA7 HETFR
Q9IA25;
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HXA7_HETFR
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                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWED outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                 MEDLINE=96032352; PubMed=7557438;

MEDLINE=96032352; PubMed=7557438;

Gaur A.F., Lemanski L.F., Dube D.K.;

Gaur A.F., Lemanski L.F., Dube D.K.;

Gaur D.F., Lemanski L.F., Down D.F.;

Gene in the Mexican axolot1 (Ambystoma mexicanum).";

Gene 162:249-253(1995).

-!- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0024; ANTENNAPEDIA.
PRINTS; PR00024; HOMBOBOX.
PRODOM; PR000101; Homeobox; 1.
SMART; SM00039; HOX; 1.
PROSITE; PS00037; HOMBOBOX 1; 1.
PROSITE; PS000132; ANTENNAPEDIA; 1.
PROSITE; PS00013; HOMBOBOX 2; 1.
TRANSCIPE; PS00013; HOMBOBOX 2; 1.
Transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 92; DB 1; Length 148; 100.0%; Pred. No. 8.4e-08; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 132 HOMEOBOX.
148 AA; 16758 MW; C1893F0ED9BF5086 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                  Homeobox protein Hox-A5 (Fragment).
                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, PO2833; ISAN.
TRANGFAC, T03305; -.
InterPro; IPRO01827; Antennapedia.
InterPro; IPRO01356; Homeobox.
                                                                                                                                                                            Ambystoma mexicanum (Axolot1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 ROIKIWFONRRMKWKK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U19238; AAA91634.1; -.
PIR; PC4071; PC4071.
1 ROIKIWFONRRMKWKK 16
                        52 ROIKIWFONRRMKWKK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00046; homeobox; 1
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Best Local Similarity 100.0
Matches 16; Conservative
                                                                                      STANDARD;
                                                                                                                                                                                                                             NCBI_TaxID=8296;
                                                                                    HXAS AMBME
P50208;
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DNA_BIND
SEQUENCE
                                                                           HXAS_AMBME
                                                             RESULT 20
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153 AA.

PRT;

STANDARD;

HXC6_SHEEP ID _HXC6_SHEEP

RESULT 21

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                                                                                                                                                                                                                                                                                                            Cosby N.C., Hernandez-Ledezma J., Mathialagan N., Roberts R.;
Submitted (Apd.1995) to the EMBL/Genbank/DDBD databases.
-!- PUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
Heterodontidae; Heterodontus.
                                                                                                                                               Vis aires (Sireca).
Eukaryota; Metazza; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Buthazza; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0025; ANTENNAPEDIA.
PRINTS; PRO0024; HOMBOBOX.
ProDom; PD0000104; HOMBOBOX; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMBOBOX 1; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
HOMBOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 92; DB 1; Length 153; Pred. No. 8.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291E24399159621E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTP-TYPE HEXAPEPTIDE.
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-A7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ARG.
POLY-GLY.
GLU/LYS-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 118 HON
86 89 POI
126 19 POI
139 153 GIL
153 AA; 17804 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 RQIKIWFQNRRMKWKK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
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HSSP; P02833; 9ANT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match.
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                   Ovis aries (Sheep)
                                                                                                                                                                                                                             NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7792;
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HXB7 BOVIN
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SEQUENCE
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   SO THE SERVICE COURSE SERVICE SERVICE COURSE SERVICE SERVICE SERVICE COURSE SERVICE SE
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                                                                                                                                                                                                                                                                                      **SIMILARITY: LOCATION: Nuclear (By similarity).

-! SUMILARITY: Belongs to the Antp homeobox family.

-! SIMILARITY: Belongs to the Antp 
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                      SEQUENCE FROM N.A.

MEDLINE=20144096; Pubmed=10677514;

Kim C.B., Anmenya C., Bailey W., Kawasaki K., Mezey J., Miller W.,

Kim C.B., Anmenya C., Bailey W., Kawasaki K., Mezey J., Miller W.,

Minoshima S., Shimizu N., Wagner G., Ruddle F.;

"Hox cluster genomics in the horn shark, Heterodontus francisci.";

"Hox cluster genomics in the horn shark, Heterodontus francisci.";

Proc. Natl. Acad. Sci. U.S.A. 97:1655-1660(2200).

-!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=8821489; PubMed=2452727;
Condite B.G., Harland R.M.;
"Posterior expression of a homeobox gene in early Xenopus embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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PRINTS; PRO0024; HOMEOBOX.
PRODOM; PRO001010; HOMEOBOX; 1.
PROSITE; PS00031; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50017; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 92; DB 1; Length 208; 100.0%; Pred. No. 1.2e-07; varive 0; Mismatches 0; Indels
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01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOXA7 OR XLHBOX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI; 209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF224262; AAF44645.1; -. HSSP; P02833; 9ANT.
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J. Cell. Biochem. 79:210-221(2000).
-!-FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
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Bostrom K., Tintut Y., Kao S.C., Stanford W.P., Demer L.L.;
HOXB7 overexpression promotes differentiation of C3H10T1/2 cells to
smooth muscle cells.";
                                                                                                                        a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-!- SUBCELULAR LOCATION NOLSER.
-!- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN THE POSTERIOR MESODERM AND ECTODERM OF EARLY XENOPUS EMBRYOS.
-!- SIMILARITY: Belongs to the Antp homeobox family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR00187; Antennapedia.
InterPro; IPR00185; Homeobox.
InterPro; IPR00185; Homeobox.
InterPro; IPR00185; Homeobox.
I.
PRINTS; PR00025; ANTENNARBEDIA.
PRINTS; PR00024; HOMEOBOX.
PROFFICE PS00027; HOMEOBOX.
PROSITE; PS00027; HOMEOBOX. 1.
PROSITE; PS00027; HOMEOBOX. 1.
PROSITE; PS00032; ANTENNAREDIA; I.
PROSITE; PS00071; HOMEOBOX. 2, 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M24752; AAA49753.1; EMBL; M24752; AAA49753.1; -
EMBL, X07103; CAA30124.1; ALT_INIT.
BYR, P02833; A43553.
TRANSFAC; T01704; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 ROIKIWFONRRMKWKK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ROIKIWFONRRMKWKK 16
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Best Local Similarity 100.0
Matches 16, Conservative
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Job time : 9.8 secs
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SEQUENCE
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                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the between absoinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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"Lymphoid expression and TATAA binding of a human protein containing
an Antennapedia homeodomain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-87260899; PubMed=2885844;
Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.,
Zappavigna V., D'Esposito M., Pannese M., Russo G., Boncinelli E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                             HSSP; P02833; 1HOM.
InterPro; 1FR001287; Antennapedia.
InterPro; 1FR001286; Homeobox.
Pfan; PP00046; homeobox.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR000024; HOMEOBOX.
PRODON; PD000010; Homeobox.
SMART; SM00389; HOX; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00032; HOMEOBOX 2; 1.
PROSITE; PS00017; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                 ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peschle C.;
"Two human homeobox genes, cl and c8: structure analysis and expression in embryonic development.";
Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918(1987).
                                                                                                                                                                                                                                                                                                                                                                       Score 92; DB 1; Length 217;
Pred. No. 1.3e-07;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K., Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;
                                                                                                                                                                                                                                                                                                          ANTP-TYPE HEXAPEPTIDE,
HOMEOBOX.
GLU-RICH (ACIDIC).
; 4E0EB4C534F08884 CRC64;
            -!- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HXB7_HUMAN STANDARD; PRT; 217 AA. P09629; Q15857; 10. Created) 01-AR-1989 (Rel. 10, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) HOXB7 OR HOXE? (HOX-2C) (HHO.CI)
                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 119-217 FROM N.A.
MEDLINE=90046832; PubMed=2573064;
-!- SUBCELLULAR LOCATION: Nuclear,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 98-217 FROM N.A.
MEDLINE-91329816; PubMed=1678287;
                                                                                                                                    EMBL; AF200721; AAF17552.1; -.
                                                                                                                                                                                                                                                                                                                                                23940 MW;
                                                                                                                                                                                                                                                                                                                                                                        100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                179 ROIKIWFONRRMKWKK 194
                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                        1 RQIKIWFQNRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                 Franscription regulation.
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                                                                                                                                                                                                                                                                                                                      137
210
217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                        ONA BIND
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HXB7_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                           -!- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-!- SUBCELLUAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the Antp homeobox family.
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"Lineage-restricted expression of homeobox-containing genes in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003700; F:transcription factor activity; NAS.
GO; GO:0007275; P:devalopment; NAS.
GO; GO:00061575; P:regulation of transcription, DNA-dependent; NAS.
InterPro; IPR001827; Antennapedia.
InterPro; IPR0011856; Homeobox.
                                                                                                       SEQUENCE OF 137-202 FROM N.A.
MEDLINE=90215256; PubMed=2576652;
Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
"Organization of human class I homeobox genes.";
Genome 31:745-756(1989).
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PROSITE; PS00032; ANTENNAREDIA; 1.
PROSITE; PSS0071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
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H -> F (IN REF. 2).
K -> N (IN REF. 1).
T -> A (IN REF. 1).
T -> A (IN REF. 1).
GPG -> APA (IN REF. 2).
W, 995D9FF700B576A7 CRC64;
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                              hematopoietic cell lines.";
Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989)
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EMBL; A4976; AAB19469.2; -.
EMBL; M30598; AAA3605.1; -.
PIR; A26030; WJHU2C.
HSSP; P02833; JHOM.
TRANSFAC; T01734; -.
Genew; HGNC:5118; HOXB7.
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PRINTS; PRODO24; HOMBOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
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217 AA;
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Matches 16; Conserv
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October 1, 2004, 11:56:56; Search time S0.8 Seconds (without alignments) 99.376 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                             1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 100 summaries
                                                                        OM protein - protein search, using sw model
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1: sp archea:*
2: sp_bacteria:*
3: sp fungi:*
4: sp_human:*
5: sp_numan:*
5: sp_mammal:*
5: sp_mammal:*
5: sp_mammal:*
5: sp_mammal:*
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sp_virus:*
sp_vertebrate:*
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Maximum DB seq length: 200000000
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92
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Perfect score:
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                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:* sp_bacteriap:*

sp_archeap:*

<b>ហ</b> ុជា	Description	Q86fu0 drosophila	057368 brachydanio	Q80wh6 rattus sp.	057359 brachydanio	Q9pvr9 oryzias lat	Q27413 ctenodrilus	Q23743 ctenodrilus	Q26407 ctenodrilus	Q9pvr8 oryzias lat	Q9y188 priapulus c	Q25208 junonia coe	057362 brachydanio	Q8wrm9 lithobius a	Q9nb42 anopheles g	Q9pvr5 oryzias lat	077143 archegozete
SUMMARIES			8	91	6.0	6	_		~	88	<u> </u>	<b>~</b>	2	•	٥,	5	~
SU	<u>.</u>	Q86FU0	057368	080WH6	057359	Q9PVR9	227413	223743	226407	Q9PVR8	Q9Y188	225208	057362	28WRM9	29NB42	Q9PVR5	077143
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	Length	33	39	42	43	46	51	51	51	57	58	28	28	53	53	59	9
, ak	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	92	92	92	92	92	92	92	92	92	92	92	92	92	92	92	92
	Result No.	п	7	e	4	S	9	7	αο	o,	10	11	12	13	14	15	16

Q80wh7 rattus sp. Q80wh7 rattus sp. Q80g15 petromyzon Q8gg15 petromyzon Q8gg15 petromyzon Q8gg17 petromyzon Q9pws oryzias lat Q9ug24 lingula ung Q9ug29 mremia san Q9pws oryzias lat Q9ug29 mremia san Q9ug29 paralichthy Q8gfw4 lampetra intes Q9fwt lithobius f Q9fwt lithobius geng Q9ug25 lingula ung Q8wg10 euprymna sc Q9gg11 petromyzon geng G9fwt lithobium c Q8wg10 euprymna sc Q9gg11 petromyzon geng G9fwg1 euprymna sc Q9wg25 lineus sang Q9wg251 lineus sang	Q17139 branchiosto Q26498 schistocerc Q8wrm8 lithobius a Q8jzw2 mus musculu Q94575 heliocidari Q05011 artemia san Q4258 ethmostigmu Q801b5 latimexia m Q4268 acanthokara Q801d0 latimexia m Q65009 artemia san Q61679 mus musculu
0 077139 0 113 Q800MH4 0 113 Q800MH4 0 113 Q800GL2 0 13 Q800GL3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Q801a6 latimeria m
Q8jh54 brachydanio
Q801c0 latimeria m
                       Q24681 dugesia tig.
Q96bq6 homo sapien
Q9xy03 dugesia jap
Q90vz9 gallus gall
O18313 ciona intes
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    076844 cupiennius
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HOXC5A OR HOXC5.

Brachydanio rerio (Zebrafish) (Danio rerio).

Brachydanio rerio (Zebrafish) (Caniata, Vertebrata, Euteleostomi, Eutenopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.

NCBI_TAXID=7955,
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600, GO:0005634; C:nucleus; IEA.
GO; GO:0003700; Franscription factor activity; IEA.
GO; GO:0003700; F:regulation of transcription, DNA-dependent; IEA.
InterPro.; PR001356; Homeobox.
PRINTS; PR00124; HOMEOBOX.
PRODOUM; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-93292933; PubMed-8099892;
Randazzo F.M., Seeger M.A., Huss C.A., Sweeney M.A., Cecil J.K.,
Kaufman T.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila pseudoobscura (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
NCBI_TaxID=7237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural changes in the antennapedia complex of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 92; DB 5; Length 33; 100.0%; Pred. No. 1.3e-07; Live 0; Mismatches 0; Indels
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33 AA; 3963 MW; D78E37ED81FD45DF CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                       33 AA.
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                  Q24681
Q96BQ6
Q9XY03
Q90VZ9
O18313
Q8BJW4
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Q8JH54
Q801C0
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Best Local Similarity 100.0
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  pseudoobscura."
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SEQUENCE
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OCCOORDINATION
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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MEDLINE=95217128; PubMed=7702549;
MEDLINE=95217128; PubMed=7702549;
MEDLINE=95217128; PubMed=7702549;
MEDLINE=95217128; PubMed=7702549;
MEDLINE=529; MEDLINE=1806(1994).
MEDLINE: SCS209; AR731864.1; -..
GO; GO:0005634; C:nucleus; IEA.
GO; GO:00056355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO01047; HTH lambrepressr.
InterPro; IPRO01047; HTH lambrepressr.
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Last annotation update)
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100.0%; Pred. No. 1.6e-07;
tive 0; Mismatches 0;
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PRINTS; PRODO31; HTHREPRESER.
PRODON; Homeobox; 1.
SWART; SMO039; HOX; 1.
PROSITE; PSO0027; HOMEOBOX 1; 1.
PROSITE; PSSO071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 ROIKIWFONERMKWKK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 24, (TrEMBLrel. 25,
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Best Local Similarity 100.
Matches 16; Conservative
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01-OCT-2003
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GO; GO:0005634, C:nucleus; IEA.
GO; GO:0005634, C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003700; F:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
PFam; PF00046; homeobox; 1.
ProDom; PD000101, Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; FS00027; HOMEOBOX. 1; 1.
PROSITE; PS00027; HOMEOBOX. 1; 1.
DNA-Dinding; Homeobox; Nuclear protein.
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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Terebellida; Ceenodrilidae; Ctenodrilus.
NCBI_TaxID=40316;
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MEDLINE=94356262; PubMed=7915607;
Dick M.H., Buss L.W.;
"A PCR-based survey of homeobox genes in Ctenodrilus serratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 92; DB 13; Length 46; 100.0%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 92; DB 5; Length 51; 100.0%; Pred. No. 2e-07; tive 0; Mismatches 0; Indels
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Dick M.H., Buss L.W.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLUAR LOCATION: NUCLEAR (BY SIMILARITY).
-- SUBCELLUAR LOCATION: NUCLEAR (BY SIMILARITY).
-- EMBL; U26629; AAC46851.1; -- EMBL; ST6226; AAB31777.1; -- HSSP; P02835; PAB31777.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                46 AA; 5955 MW; 6039999ED4294DD3 CRC64;
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Last annotation update)
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InterPro; IPR00047; HTH_lambrepressr.
Pfam; PF00046; homeobox; 1.
PRIMTS; PR00014; HOMEOBOX;
PRINTS; PR00031; HTHEPRESSR.
ProDom; PD00010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00071; HOMEOBOX 1; 1.
NAM.-binding; Homeobox; Nuclear protein.
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Mol. Phylogenet. Evol. 3:146-158(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
LOXS ORTHOLOG homeobox (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 16; Conservative
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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ARO BRADER AND BRANCH 
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"Zebrafish hox genes: genomic organization and modified colinear
"Zebrafish hox genes: genomic organization and modified colinear
"Zebrafish hox genes: genomic organization and modified colinear
"Experience of the EMBL'Genbank/DDBJ databases."

"Submitted (ANG-1997) to the EMBL'Genbank/DDBJ databases."

"I SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

"EMBL' Y14556; CAA74861.1, -
"SEMBL' Y14556; CAA74861.1, -
"SEMBL' ZELN; ZBGENE-000823-6; hoxb5b.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:000555; P:regulation of transcription, DNA-dependent; IEA.

RO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

RO; GO:000635; P:MOMEOBOX.

R PRIORIS; PRS00027; HOMEOBOX.

R PROSITE; PS50027; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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Ukyayota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleoostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha;
Beloniformes, Adrianichthyidae, Oryzinae, Oryzias.
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Kondo S., Naruse K., Shima A.;

"Hox genes of the medakafish Oryzias latipes.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-! - SUBCELLUAR LOCATION: NUCLEAR (BY SIMILARITY).

EMBL; AB026960; BAA86243.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 AA; 5050 MW; 53034C37F3DFA596 CRC64;
                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
HOXCSA (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio)
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NON TER

SEQUENCE 43 AA; 5050 MW; 53034C37F31
                                                                                                                                                                                                                                                                                                           Created)
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                                                  01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                            Hoxas protein (Fragment).
HOXBSB OR HOXAS.
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                                                                                                                                                                                                                                     PRELIMINARY;
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nes 16; Conservative
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Local Similarity
les 16; Conserva
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006350; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; HTH lambrepressr.
Pfam; PF00046; HTH lambrepressr.
PRINTS; PR00044; HOMEODOX; I.
PRINTS; PR00031; HTHREPRESSR.
PRINTS; PR00031; HTHREPRESSR.
PRODOM; PD0001001; HOMEODOX; 1.
PROSITE; PS00037; HOMEODOX; 1.
PROSITE; PS00037; HOMEODOX; 2.
                                                                                                                                                                                                                                                                                                   Eukaryota; Merazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Terebellida; Ctenodrilidae; Ctenodrilus.
NCBI_TaxID=40316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Annelida, Polychaeta, Palpata, Canalipalpata,
Terebellida; Ctenodrilidae, Ctenodrilus.
NCBL_TaxID=40316;
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Dick M.H., Buss L.W.;
"A PCK-based survey of homeobox genes in Ctenodrilus serratus (Annelida: Polychaeta).";
Mol. Phylogenet. Evol. 3:146-158(1994).
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20.0%; Score 92; DB 5; Length 51;

Best Local Similarity 100.0%; Pred. No. 2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Dick M.H., Buss L.W.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; U26627; AA-46849.1; --
HSSP; P02833; 9ANT.
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51 AA; 6533 MW; 9EDB50C927FBCBDS CRC64;
                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Deformed ortholog homeobox (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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MEDLINE=94356262; PubMed=7915607;
                              23 RQIKIWFQNRRMKWKK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ROIKIWFONRRMKWKK 16
1 RQIKIWFQNRRMKWKK 16
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Q23743;
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Gaps
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Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                    GO; GO:0005634, C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001355; Homeobox.
Pfam; PF00046; homeobox: 1.
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Dick M.H., Buss L.W.;
"A PCT-based survey of homeobox genes in Ctenodrilus serratus
(Annelida: Polychaeta).";
Mol. Phylogenet. Evol. 3:146-158(1994).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
BMSL; 376411, AN BMST75-1; -.
HSSP; P02833; 9ANT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 92; DB 5; Length 51; 100.0%; Pred. No. 2e-07; tive 0; Mismatches 0; Indels
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Krondo S., Naruse K., Shima A.;
Krondo S., Naruse K., Shima A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; BAD02631, BAA86244.1;
-- HSSP, P02833; 1HOM.
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Probom; PRO00010; Homeobox; 1.

SMART; SM0389; HOX; 1.

PROSITE; PS50071; HOMEOBOX 1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

PROFITE; PS50071; HOMEOBOX 2; 1.

NOM - binding; Homeobox; Nuclear protein.

NON TER

SEQUENCE 57 AA; 6891 MW; 54A6430320F68C04 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                               Pfam, Pr00046, homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESR.
ProDom; PD000010; Homeobox; 1.
SWART; SW00389; HOX; 1.
PR0SITE; PS00027; HOMEOBOX 1; 1.
PR0SITE; PS00027; HOMEOBOX 1; 1.
DR0SITE; PS00027; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
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A PART REPORT OF THE PROPERTY 
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
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Matches 16; Conservative
                                       EMBL; L42135; AAA68461.1;
PIR; S58850; S58850.
HSSP; P02833; 1HOM.
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Best Local Similarity
Matches 16; Conserv
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GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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MEDLINE=55075456; PubMed=7840822;
Marren R.W., Nagy L., Selegue J., Gates J., Carroll S.;
Warren R.W. of homeotic gene regulation and function in files and butterflies.";
Nature 372:458-461(1994).
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Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Dirrysia;
Papilionoidea; Nymphalidae; Nymphalinae; Junomia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 92; DB 5; Length 58; Lindty 100.0%; Pred. No. 2.3e-07; Conservative 0: Midmatar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Priapulus caudatus.
Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulus.
NCBI_TaxID=37621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 AA; 7323 MW; 572F30DA57C9A613 CRC64;
                                                                                                                                                                                                                                                                                                                        OSY188;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
HB1 homeodomain protein (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Antennapedia protein (Fragment).
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                                                                                                                                                                                                                                                                                             PRT;
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PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; HOMEObox; 1.
SMART; SM00389; HOX; 1.
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                                                             23 RQIKIWFQNRRMKWKK 38
        1 ROIKIWFONRRMKWKK 16
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es 16; Conserv
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RESULT 11

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Matches

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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T03635; -
TRANSFAC; T03635; -
ZFIN; ZDB-GENE-000329-2; hoxb7a,
GO; GO:0005634; C.nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeobox.
PF00046; homeobox: 1.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003563; C:nucleus; IEA.
GO; GO:0000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
InterPro; IPR001047; HTH lambrepressr.
Pf00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.

Prince V.E., Joly L., Ekker M., Ho R.K.;
"Zebrafish hox genes: genomic organization and modified colinear expression patterns in the trunk.";
Submitted (ANG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 92, DB 5; Length 58; 100.0%; Pred. No. 2.3e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                             PRINTS; PRO0024; HOMEDBOX.
PRINTS; PRO0024; HOMEDBOX.
PRINTS; PRO0013; HTHREPRESSR.
PRODON; PRO0021; HOMEDBOX; 1.
PROSITE; PSO0027; HOMEDBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
NON TER 1 1 1
NON TER 58 58
SEQUENCE 58 AA; 7583 MW; BD69B4875BAE565E CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
HOXb7 Droctein (Fragment)
HOXB7 OR HOXB7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 AA.
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PRINTS; PRO0031; HTHREPRESSR.
ProDom; PD0000010; Homeobox; 1.
PROSITE; PS00027; HOMEOBOX.1; 1.
PROSITE; PS50071; HOMEOBOX.2; 1.
DNA-binding; Homeobox; Nuclear protein.
NON TER.
SEQUENCE 58 AA; 6863 MW; 41EA6F1448BDA
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-!- SUBCĒLLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AF269155; AAF91400.1; -.
HSSP; P02833; 1SAN.
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es 16; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM M.A.

Hughes C.L., Kaufman T.C.;

"Exploring the myriaped body plan: expression patterns of the ten Hox genes in a centipede ";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).

EMBL; AF434996; AA136901.1; -..

EMBL; AF434996; AA136901.1; -..

GO; GO:000053700; F:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000047; HTH_lambrepressr.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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Powers T.P., Hogan J., Ke Z., Dymbrowski K., Wang X., Collins F.H.,
Kaufman T.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of the Hox cluster from the mosquito Anopheles gambiae (Diptera: Culicidae).";
Evol. Dev. 2:311-325(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Arthropoda, Myriapoda, Chilopoda,
Pleurostigmophora, Lithobiomorpha, Lithobiidae, Lithobius.
NCBI_TaxID=177213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 AA; 7093 MW; 9E60036CE0D515C1 CRC64;
                                                                                                                                                                                                                                                                                                                         01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-001-2000 (TrEMBLrel. 15, Created)
01-001-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                       PRT;
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SAMRAT; SR00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
                                                                                       14 ROIKIWFONRRMKK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ROIKIWFONRRMKWKK 16
                                      1 ROIKIWFONRRMKWKK 16
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                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Antennapedia (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ithobius atkinsoni.
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                                                                                                                                                                                                                                                                                                    Q8WRM9;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neoperygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0005355; P:transcription of transcription, DNA-dependent; IEA.
INTEPPRO; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
PR00124; HOMEOBOX.
ProDom; PR001024; HOMEOBOX.
PROSITE; PS00027; HOMEOBOX 1:
PROSITE; PS00027; HOMEOBOX 1: 1.
PROSITE; PS00071; HOMEOBOX 1: 1.
PROSITE; PS00071; HOMEOBOX 2: 1.
NON TER 59 59
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                                                                                                                                                                                                                                                                                                       100.0%; Score 92; DB 5; Length 59; 100.0%; Pred. No. 2.3e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             SEQUENCE ' 59 AA; 7621 MW; C38A2505A81D9952 CRC64;
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Last annotation update)
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PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
NON TEX 1
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NCBI_TaxID=10118;
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MEDLINE=98393703; PubMed=9724762;
MEDLINE=98393703; PubMed=9724762;
Telford M.J., Thomas R.H.;
Texpression of homeobox genes shows chelicerate arthropods retain their deutocerebral segment.";
Their deutocerebral segment.";
Proc. Natl. Acad. Sci. U.S.A. 95:10671-10675(1998).
L. SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AF071407; AAC35936.1; -.
HSSP; PO2833; 1SAN.
R GO; GO:0005349; Cinucleus; IEA.
R GO; GO:00053700; F:transcription of transcription, DNA-dependent; IEA.
R DO:0003700; F:transcription of transcription, DNA-dependent; IEA.
R InterPro; IPR00195; Homeobox.
R PRINTS; PR000024; HOMEOBOX.
R PRINTS; PR000024; HOMEOBOX.
R PRODEN; S000029; HOMEOBOX; 1.
R RPACITE; PS00027; HOMEOBOX; 1.
R PROSITE; PS00027; HOMEOBOX 1; 1.
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MEDLINE=98393703; PubMed=9724762;

Telford M.J., Thomas R.H.;

Telford M.J., Thomas R. R.H.;

"Expression of homeobox genes shows chelicerate arthropods retain their deutocerebral segment.";

Proc. Natl. Acad. Sci. U.S.A. 95:10671-10675(1998).

-!- SUBCELLULAR LOCATION: VUCLEAR (BY SIMILARITY).

EMBL; AF071403; AAC35932.1; -.
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Acariformes; Sarcoptiformes; Oribatida; Desmonomata;
Trhypochthonicidea; Trhypochthoniidae; Archegozetes.
NCBI_TaxID=66560;
                                                                                                                                                                                                                        Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari,
Acariformes, Sarcoptiformes, Oribatida, Desmonomata,
Trhypochthonioldea, Trhypochthonidae, Archegozetes.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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NON TER 60 60
                                          PRT;
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                                                                                                                                                        Sex combs reduced (Fragment)
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Best Local Similarity 100.0°
Matches 16; Conservative
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                                                                                                                                                                                                    Archegozetes longisetosus.
                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                 NCBI TaxID=66560;
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                                       077143
RESULT 16
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R HSSP; P02833; 1SAN.

R GO; GO:0005334; C:nucleus; IEA.

R GO; GO:000536; F:rrancleus; IEA.

R GO; GO:000635; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR00135; HTM-lambrepressr.

P Fam; PF00046; homeobox;

R PRINTS; PR00031; HTM-EPRESSR.

R PRINTS; PR00031; HTM-EPRESSR.

R PRINTS; PR000101; HOMEOBOX.

R PRODOM; PD000010; HOMEOBOX.

R PROSTIE; PS00017; HOMEOBOX.

T NON_TER 60 60

SEQUENCE 60 AA; 7755 MW; 32678A250BBDE74 CRC64;
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MEDILINE=95217128; PubMed=7702549;

MEDILINE=95217128; PubMed=7702549;

MEDILINE=95217128; PubMed=7702549;

Cloning of rat homeobox genes.";

ENGLY, S76287; AAP31863.1;

ENGLY, GO:0005634; C:nucleus; IEA.

GO:0005634; C:nucleus; IEA.

GO:0005634; C:nucleus; IEA.

GO:0005635; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR00135; HOMEObox.

InterPro; IPR00135; HOMEOBOX.

INTERPRO; PR00024; HOMEOBOX.

PRINTS; PR00024; HTHEPRESSR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
HOX-A|HOX-1 (Fregment).
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100.0%; Pred. No. 2.4e-07;
tive 0; Mismatches 0;
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SMART, SM00389; HOX; 1.
PROSITE, PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ROIKIWFONRRMKWKK 16
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Best Local Similarity 100.00
Best Local Similarity 100.00
Best Local Similarity 100.00
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Best Local Similarity 100.0
Matches 16; Conservative
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RARANTTS
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                                                                                                                                                                                                                                             Rattus sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95217128; PubMed=7702549; MEDLINE=95217128; PubMed=7702549; MEDLINE=95217128; PubMed=7702549; MEDLINE=95217128; PubMed=7702549; "Cloning of rat homeobox genes."; "Cloning of rat homeobox genes."; Biochem. Genet. 32:351-360(1994). "Biochem. Genet. 32:351-360(1994). "Genet. 32:351-360(1994). "Genet. 32:351-360(1994). "Genet. 32:351-360(1994). "Genet. 32:351-360(1994). "Genet. 32:351-360(1994). "EA. Go, GO:000355; Pregulation factor activity; IEA. GO; GO:000355; Pregulation of transcription, DNA-dependent; IEA. InterPro; IPR000047; HTH lambrepressr.
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-1. Exp. 2010.0:0-0(2002).
-1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
GO, GO:0003709; F. C. nucleus; I.EA.
GO, GO:0003709; F. transcription factor activity; IEA.
GO; GO:000355; P. regulation of transcription, DNA-dependent; IEA.
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Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Irvine S.Q., Carr J.L., Bailey W.J., Kawasaki K., Shimizu N.,
Amemiya C.T., Ruddle F.H.;
"Genomic analysis of Hox clusters in the sea lamprey Petromyzon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AA; 7842 MW; 3407ED69B4874816 CRC64;
                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
HOX-B HOX-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Interpro; IPR000047; HTH lambrepressr.
Pfam; PF000046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ROIKIWFONRRMKWKK 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                              PRELIMINARY;
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                              Q80WH4
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Q80WH4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 marinus.";
-1 Exp. 2001.0:0-0(2002).
-1 SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

EMBL; AF410916; AAM19474.1; --
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; P:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
Interpro; IPR001356; Homeobox.
Interpro; IPR001047; HTH-lambrepressr.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

Petromyzontiformes; Petromyzontidae; Petromyzon.
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0
                                                                                                                                                                                                          100.0%; Score 92; DB 13; Length 60; 100.0%; Pred. No. 2.4e-07; Live 0; Mismatches 0; Indels
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Prodom, PD000010; Homeobox; 1.

PROSITE; SM00139; HOX; 1.

PROSITE; PS00027; HOMEOBOX_1; 1.

PROSITE; PS50071; HOMEOBOX_2; 1.

HOMEOBOX; DNA-binding; Nuclear protein.

NON_TER 1 1 1

NON_TER 6 60

SEQUENCE 60 AA; 7717 MW; E1S0F172FD751F3C CRC64;
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NON TER 60 60
SEQUENCE 60 AA; 7863 MW; 1334F475E49E47FE CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TEMBLrel. 21, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
HoxK6 homeobox (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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PRINTS; PRO00131, HTHERERESSR.
Probom; PD00010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Best Local Similarity 100.0
Matches 16, Conservative
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080GL3;
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QBQGL6
ID QBQGL0
AC Q8QGL0
DT 01-JU
DT 01-JU
DT 01-JU
DE HOXK6
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60 60 60 AA; 7863 MW; 1334F475E49E47FE CRC64;

NON TER SEQUENCE

us-09-830-779-7.rspt

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Gaps
                                                                                                                                                      marinus.",

"I Exp. 2501. 0:0-0(2002).

-1 - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

EMBL, AF410913, AAM19471.1;

EMBL, AF410913, AAM19471.1;

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0007100; F:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001356; Homeobox.

InterPro; IPR00147; HTH_lambrepressr.
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
GO, GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003750; F:transcription of transcription, DNA-dependent; IEA.
InterPro; IPRO01355; Homeobox.
InterPro; IPRO0147; HTH_lambrepressr.
Pfam; PF00046; homeobox; 1.
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Q8QGL2;

O1-UTN-2002 (TrEMBLrel. 21, Created)

O1-UTN-2003 (TrEMBLrel. 24, Last sequence update)

O1-UTN-2003 (TrEMBLrel. 24, Last annotation update)

HOXN7 homeobox (Fragment).

Fetromyzontifermes; Petromyzontidae; Petromyzon.

NCBI_TaxID=7757;
Petromyzon marinus (Sea lamprey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Hyperoartia,
Petromyzontiformes, Petromyzontidae, Petromyzon.
                                                                                                      Irvine S.Q., Carr J.L., Balley W.J., Kawasaki K., Shimizu N., Amemiya C.T., Ruddle F.H.; "Genomic analysis of Hox clusters in the sea lamprey Petromyzon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Irvine S.C., Carr J.L., Bailey W.J., Kawasaki K., Shimizu N., Amemiya C.T., Ruddle F.H.; "Genomic analysis of Hox clusters in the sea lamprey Petromyzon
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                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0024; HOMEOBOX.
PRINTS; PRO0011; HTHREPRESSR.
Prodom; PD000010; Homeobox; 1.
SWART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
NON_TER
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PROSITE; PS0027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEObox; DNA binding; Nuclear protein.
NON_TER
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PRINTS; PR00031; HTHREPRESSR.
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                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE
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Q8QGL2
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TAYING S.Q., CART J.L., Bailey W.J., Kawasaki K., Shimizu N., Amemiya C.T., Ruddle F.H.;

"Genomic analysis of Hox clusters in the sea lamprey Petromyzon marinus.";

"Genomic analysis of Hox clusters in the sea lamprey Petromyzon marinus.";

"GENELLIAR LOCATION: NUCLEAR (BY SIMILARITY).

EMBL; AF410911; AAM19469.1; -.

RO; GO:0003700; Firmanscription factor activity; IEA.

GO; GO:0003700; Firmanscription function, DNA-dependent; IEA.

RO; GO:0003700; Firmanscription franscription, DNA-dependent; IEA.

RO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

RO; GO:0003100; Firmanscription functions.

RR CO; GO:000310; HTHERERESS.

PRINTS; PRO0004; HOMEOBOX.

PRINTS; PRO0010; HOMEOBOX.

RR PROSITE; PSO0017; HOMEOBOX.

RR
                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HoxG4 homeobx. (Fragment).

Petromyzon marinus (Sea lamprey).

Bukaryota, Metazoa, (Chordata; Craniata; Vertebrata; Hyperoartia;

Petromyzontiformes; Petromyzontidae; Petromyzon.
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HoxJ5 homeobox (Fragment).

Betromyzon marinus (Sea lamprey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

Petromyzontiformes; Petromyzontidae; Petromyzon.
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Score 92, DB 13; Length 60;
Pred. No. 2.4e-07;
; Mismatches 0; Indels
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08GGL7;
01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        60 AA.
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   Query Match 100.0%; Score 92, DB Best Local Similarity 100.0%; Pred. No. 2.4e Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                        1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                  43 ROIKIWFONRRMKWKK 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
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Q8QGL7
                                                                                                                                                                                                                                                                                                       RESULT 24
Q8QGL8
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RA Irvine S.O., Carr J.L., Bailey W.J., Kawasaki K., Shimizu N.,
RA Amemiya C.T., Ruddle F.H.;
RT "Genomic analysis of Hox clusters in the sea lamprey Petromyzon
RT "arzinus.";
J. Exp. Zool. 0:0-0(2002).
CC
CC
CC GOOODSGAR C.T. CARTON: NUCLEAR (BY SIMILARITY).
DR GO, GOOODSGAR C. CARTON: NUCLEAR (BY SIMILARITY).
DR GO, GOOODSGAR C. CARTON: NUCLEAR (BY SIMILARITY).
DR GO, GO:00003700; F:transcription feator activity; IEA.
DR GO, GO:0003700; F:transcription of transcription, DNA-dependent; IEA.
DR GO, GO:0004376; Homeobox.
DR RINITS; PRO0124; Homeobox.
DR RINITS; PRO0124; Homeobox.
DR RINITS; PRO0124; Homeobox.
DR RYNITS; PRO0124; Homeobox.
DR RYNITS; PRO0127; ```

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Gencore version 5.1.6

Copyright (c) 1993 - 2004 Compagen Ltd.

OM protein - protein search, using sw model

Run on: October 1, 2004, 11:56:15; Search time 63.2 Seconds

Title: US-09-830-779-8

Perfect score: 75
Sequence: 1 MEKVOYLTRSAIRRAS 16
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1586:107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586:107

Minimum DB seq length: 00
Maximum Match 100*
Listing first 100 summaries

Database: 1 Geneseq_29Jan04:*
1 geneseqp2000s:*
2 geneseqp2000s:*
3 geneseqp2000s:*
5 geneseqp2000s:*
6 geneseqp2000s:*
7 geneseqp2000s:*
7 geneseqp2000s:*
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7 geneseqp2003s:*
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8 geneseqp2003s:*
8 geneseqp2003s:*
8 geneseqp2003s:*
8 geneseqp2003s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |       | Description  | Aay71009 Human Pho |          | Н        | 'n       | Aay71003 Human mut | Aay71002 Human Pho | Abp06592 Human ORF | _        | Ade45170 Rabbit SE | Ade45171 Rat SERCA | Ade45167 Human SER | Aay71019 H6 tagged | Hex      |          | 8 Pig    | Ade45169 Dog SERCA |          | Aay71013 Penetrati |          | Ade45173 Chicken S | Aay71018 H6 tagged | Hun      | Aay71004 Human mut | Aay71007 Human mut | Adc87928 Ribosomal |
|-----------|-------|--------------|--------------------|----------|----------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|--------------------|----------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|
| SUMMARIES |       | dī           | AAY71009           | AAY71012 | AAY71011 | ADE45175 | AAY71003           | AAY71002           | ABP06592           | ADE45172 | ADE45170           | ADE45171           | ADE45167           | AAY71019           | AAY71017 | AAY71006 | ADE45168 | ADE45169           | AAY71014 | AAY71013           | ABB79404 | ADE45173           | AAY71018           | AAY71005 | AAY71004           | AAY71007           | ADC87928           |
|           |       | DB           | ! ~                | m        | m        | œ        | 3                  | m                  | S                  | 89       | œ                  | 80                 | œ                  | m                  | m        | 3        | 00       | 00                 | m        | <b>(</b> 1)        | ស        | œ                  | 'n                 | L,)      | m                  | 'n                 | ٢                  |
|           |       | Match Length | 16                 | 35       | 36       | 36       | 52                 | 52                 | 52                 | 52       | 52                 | 52                 | 52                 | 79                 | 79       | 52       | 25       | 52                 | 35       | 36                 | 52       | 52                 | 79                 | 52       | 52                 | 52                 | 116                |
|           | * 6   | Match        | 100.0              | 100.0    | 100.0    | 100.0    | 100.0              | 100.0              | 100.0              | 00       | 100.0              | 100.0              | 100.0              | 100.0              | 100.0    | 96.0     | 0.96     | 96.0               | 94.7     | 94.7               | 94.7     | 94.7               | 94.7               | 'n       |                    | 88.0               | 54.7               |
|           |       | Score        | 75                 | 75       | 75       | 75       | 75                 | 75                 | 75                 | 75       | 75                 | 75                 | 75                 | 75                 | 75       | 72       | 72       | 72                 | 71       | 71                 | 71       | 71                 | 71                 | 70       | 69                 | 99                 | 41                 |
|           | יומסק | No.          | -                  | 7        | m        | 4        | ហ                  | 9                  | 7                  | œ        | σ                  | 10                 | 11                 | 12                 | 13       | 14       | 15       | 16                 | 17       | 18                 | 19       | 20                 | 21                 | 22       | 23                 | 24                 | 25                 |

| 1187 Strept<br>1187 Strept<br>1657 TGF-be<br>1552 TGF-be<br>1552 TGF-be<br>1552 Strept<br>1741 Novel<br>163 Propio                         | 1682 Propi<br>1979 C glu<br>1260 Human<br>1491 Prote<br>1746 Human<br>1746 Human<br>1735 Prote<br>1335 Prote<br>1344 Arabi<br>1344 Arabi  | 1782 Human | Aam35032 Peptide # Abb25249 Proteind # Abb26300 Protein # Aam74917 Human bon Aam74917 Human bon Aam74917 Human bon Aam64123 Human bon Abg56613 Human bon Abg46055 Human pep Aam94331 Propining Abg3399 Protein e Abg33997 Protein e Aay3666 Fragment Ada13997 Protein e Aay3666 Fragment Ada13997 Arabidops Aag14887 Arabidops Aag14887 Arabidops Aag14887 Arabidops Abg5635 Drosophil Abu46685 Propining Abd5635 Propining Abd43247 Protein e Abg02567 Human pro Abd43247 Human pro Abd43247 Protein e Abg02591 Staphyloc Aag148818 Arabidops Abg18818 Arabidops Abg18818 Arabidops Abg18818 Arabidops Abg18818 Arabidops Abg18818 Arabidops Abg18818 Arabidops Aag18818 Arabidops Aag18888 Arabidops Aag18888 Arabidops Aag18888 Arabidops Aag18888 Arabidops Aag18888 Arabidops Aag18888 Arabidops Ar |
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Aag08266 Arabidops
Abu29277 Protein e
AAG08266
ABU29277
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ALIGNMENTS

AAY71009 standard; peptide; 16 AA AAY71009; RESULT 1 AAY71009

29-AUG-2000 (first entry)

Human Phospholamban (PLB) cargo peptide.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiamycoyre; transport peptide; penetrath; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction.

Homo sapiens.

WO200025804-A2.

11-MAY-2000

99WO-US025692. 02-NOV-1999; 98US-0106718P. 02-NOV-1998;

99US-0145883P. 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

He H, Hoshijima M, Meyer M; Minamisawa S, Dillman W, Minamisawa Wang Y, Silverman GJ; WPI; 2000-365393/31. Chien K, Scott C,

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine

Example 4; Page 50; 56pp; English.

triphosphatase.

phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic recticulum Ca 2+ Argase (SERCAZa) within catching cargo populae deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ Argase (SERCAZa) within catchingoverses. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCAZa interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the cargo peptide from human PLB amino terminal residues 1-16. It could be derived from any segment of wild type or mutant PLB protein. The cargo peptide is linked to the transport peptide by a covalent linkage The patent discloses a method for the treatment of heart failure, using 

Sequence 16 AA;

Gaps ; 0 100.0%; Score 75; DB 3; Length 16; 100.0%; Pred. No. 1e-06; live 0; Mismatches 0; Indels Ouery Match Best Local Similarity 100.0 Matches 16; Conservative

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1 MEKVOYLTRSAIRRAS 16
                                     1 MEKVOYLTRSAIRRAS 16
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AAY71012 standard, peptide; 35 AA. RESULT 2 AAY71012

AAY71012; 

(first entry) 29-AUG-2000 Penetratin-based recombinant phospholamban peptide, TAT-PLB

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a, cardiant; cardianyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; recombinant peptide; HIV; TAT protein.

Homo sapiens

Human immunodeficiency virus.

Location/Qualifiers

 .15 /note= "Corresponds to denatured human immunodeficiency virus (HIV) TAT protein" Region

Region

16.2.35 /note= "Corresponds to human phospholamban (PLB) amino terminal peptide"

WO200025804-A2

11-MAY-2000.

99WO-US025692. 02-NOV-1999; 98US-0106718P. 02-NOV-1998;

99US-0145883P. 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

He H, Hoshijima M, Meyer M; Minamisawa S, Wang Y, Silverman GJ; Dillman W, Chien K, Scott C,

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Example 5; Page 52; 56pp; English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPease (SERCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against DLB protein (contractilly). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinant peptide TAT-PLB, comprising the amino terminal end of human PLB native protein, attached to the 3' end of denatured human immunodeficiency virus (HIV), TAT protein. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the plasma membrane

Sequence 35 AA;

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Query Match

100.0%; Score 75; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels

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Gaps

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small peptide complexes and recombinant proteins, that induces the phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ArPase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinant peptide PLB-ANT, comprising the amino terminal end of human PLB native protein, attached to the 5' end of the Drosophila antennapedia (ANT) transport peptide. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the
                                                                                                                                                                                                                                                                   Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cardiac contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; recombinant peptide; fruit fly; antennapedia; ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses a method for the treatment of heart failure, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Corresponds to human phospholamban (PLB) amino terminal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21. .36
/note= "Corresponds to Drosophila antennapedia (ANT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  He H, Hoshijima M, Meyer M;
                                                                                                                                                                                                                                  Penetratin-based recombinant phospholamban peptide, PLB-ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minamisawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 52; 56pp; English.
                                                                                                                        AAY71011 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transport peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang Y, Silverman GJ;
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99US-0145883P.
1 MEKVOYLTRSAIRRAS 16
                           16 MEKVQYLTRSAIRRAS 31
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                                                                                                                                                                                               29-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-365393/31.
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                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-NOV-1999;
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                                                                                                                                                           AAY71011;
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Scott C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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                                                                                       RESULT 3
                                                                                                         1017XAA
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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, C22+ Afpease of the sarco/endplasmic reticulum, appearing as ADB45167-CA54723. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, AR-9 and/or Ar-9.13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound to binding site comprises Met-20, Lys-27 and/or Let phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-12 and/or Phe-15.7-binding site of the phospholamban, comprising administering the novel compound to stimulate the case of phospholamban, comprising administering the novel compound to stimulate the compound is not 3-benzopyzan-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the compound is companied SERCA_2. The present sequence is the cytosolic domain of human phospholamban.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                  Human; SERCA 2; phospholamban; PLB; Ca2+ ATPase \overline{o}f the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                 Gaps
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      Length 36;
  100.0%; Score 75; DB 3; Length 36
100.0%; Pred. No. 2.5e-06;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                            Human SERCA_2 inhibitor phospholamban, cytosolic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 9; 65pp; English.
                                                                                                                                                                                                                                   ADE45175 standard, peptide; 36 AA.
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                                                                                     1 MEKVOYLTRSAIRRAS 16
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Query Match
Best Local Similarity 100.0
Matches 16, Conservative
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Gaps

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100.0%; Score 75; DB 8; Length 36; 100.0%; Pred. No. 2.5e-06; Live 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Watches 16; Conserva

Sequence 36 AA;

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1 MEKVQYLTRSAIRRAS 16
1 MEKVOYLTRSAIRRAS 16
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AAY71003 standard, protein, 52 AA.

AAY71003;

(first entry) 29-AUG-2000 Human mutant phospholamban (PLB) V49A protein.

Phospholamban, PLB, human, sarcoplasmic reticulum Ca 2+ ATPase, SERCA2a, cardiant, cardiamyocyte; transport peptide, penetratin, cargo peptide, contractilin, cardiac contractility, inhibitor, cardiac disease; treatment, heart failure, myocardial dysfunction; mutant.

Homo sapiens.

Synthetic 

Location/Qualifiers Misc-difference 49

/note= "Wild type Val replaced with Ala"

WO200025804-A2

11-MAY-2000.

99WO-US025692 02-NOV-1999; 98US-0106718P 02-NOV-1998;

27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

Meyer M; He H, Hoshijima M, Minamisawa S, Silverman GJ; Dillman W, Wang Y, Chien K, Scott C,

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase

Disclosure; Page 48; 56pp; English.

small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum (a 2+ Arpase (SERCA2) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against the protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising a sense mutation (al49Ala. This mutant sequence when overexpressed in the transformed cardiomyocytes, shows increased contractility than the wild type PLB sequence The patent discloses a method for the treatment of heart failure, using

Sequence 52 AA;

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                                    Gaps
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Length 52;
100.0%; Scare 75; DB 3; Length 52 ilarity 100.0%; Pred. No. 3.7e-06; Conservative 0; Mismacches 0; Indels
Query Match
Best Local Similarity
Matches 16; Conserv
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RESULT

AAY71002 standard; protein; 52 AA.

AAY71002;

29-AUG-2000 (first entry)

Human Phospholamban (PLB) wild type protein.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction.

Homo sapiens.

Location/Qualifiers

Domain

1. .20 /label= Domain Ia /note= "Rich in alpha-helical confirmation with a net

positive charge"

Domain

21. .30 //abel= Domain Ib /note= "Cytoplasmic sector of the monomer"

/label= Domain\_II 25

Domain

/note= "Transmembrane sector made of uncharged residues responsible for stabilising the pentamer formation"

WO200025804-A2.

11-MAY-2000.

99WO-US025692. 02-NOV-1999;

02-NOV-1998; 98US-0106718P. 27-JUL-1999; 99US-0145883P.

27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

He H, Hoshijima M, Meyer M; Minamisawa S, Silverman GJ; Chien K, Dillman W., Scott C, Wang Y, S.

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Disclosure, Page 47; 56pp; English.

small peptide complexes and recombinant proteins, that induces phospholemban (PIB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ Arpase (SERAA2) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human PLB wild type protein, a potent inhibitor of SERCA2a acitivity. It primarily exists in a pentameric form. It is a medialor in the regulation of myocardial function by catecholamines through the CAMP cascade patent discloses a method for the treatment of heart failure, using

Sequence 52 AA;

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABN1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polytucloctide squares can be used in gene therapy ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, rithosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eve disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bene degenerative disorders, ulcers, ulcers, and for gut protection or regeneration and treatment of lung or liver fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psortiasis; behign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune chiroidistis;
                                                                                                    Gaps
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         100.0%; Score 75; DB 3; Length 52; 100.0%; Pred. No. 3.7e-06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ORFX protein sequence SEQ ID NO:13166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP06592 standard; protein; 52 AA.
Query Match
Best Local Similarity 100.0%; P)
Matches 16; Conservative 0;
                                                                                                                                                                                                                                         1 MEKVQYLTRSAIRRAS 16
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29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                  1 MEKVOYLTRSAIRRAS 16
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ABP06592
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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, 22.4 ATPage of the sarco/endoplasmic reticulum (a) appearing as ADE45167-ADE45173. The compound has a structure containing three of the four moietises: an electromegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site occapitation with an S2 binding site of the phospholamban cytosolic domain when the compound is bound, the S2 binding site of the phospholamban cytosolic moiety associating with an S2 binding site of the phospholamban cytosolic of main when the compound is bound, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, 1ys-27 and/or Leu-28, and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, 1ys-27 and/or Leu-28, and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is not 3-benzyl-5/-bis ([H-tetrazol-5-4)]-methyloxyl-4 methyl-2H-methyl-2H-methyl-2H-methyloxyl-4 methyl-2H-methyloxyl-4 methyl-2H-methyloxyl-4 methyl-2H-methyloxyl-4 methyloxyl-4 me
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Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
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reperfusion injury in various tissues and conditions resulting from systemic cytoKine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                       Length 52;
                                                                                                                                                                                       Query Match 100.0%; Score 75; DB 5; Length 52 Best Local Similarity 100.0%; Pred. No. 3.7e-06; Matches 16; Conservative 0; Mismatches 0; Indels
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onen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse SERCA_2 inhibitor phospholamban.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE45172 standard; protein; 52 AA.
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Yliperttula-Ikonen M,
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                                                                                                                                      Sequence 52 AA;
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WPI; 2004-019625/02.
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Query Match
Best Local Similarity
                                                                                                                                                                                                        Sequence 52 AA;
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                                                                           US6538022-B1.
                                                                                       18-FEB-1999;
                                                                                             24-SEP-1997;
                                                                                 25-MAR-2003.
                                       ADE45170;
                                                               cardiant
                                                                                                                              -ATPase.
      Matches
                           RESULT 9
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                      Rabbit; SERCA 2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
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                                                                          Gaps
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                                100.0%; Score 75; DB 8; Length 52; 100.0%; Pred. No. 3.7e-06;
                                                                        0; Indels
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.lgmann C, Lotta T, Kaivola J;
                                                100.0%; Pred. ...
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                                                                                                                                                                                                                                                             ADE45170 standard; protein; 52 AA.
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                                                                                                                      1 MEKVOYLTRSAIRRAS 16
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                                                                          16; Conservative
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Yliperttula-Ikonen M,
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Sequence 52 AA;
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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA. 2, Ca2+ Arpsae of the sarco/endoplasmic reticulum) appearing as ADB45167-CADB45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyre, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Arg-14, a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating the capture of the call argument of the call argument is not 3-benzyl-57-bis ([Hr-tetrazol-5-yl])-methyloxyl-4 call argument compound is not 3-benzyl-57-bis ([Hr-tetrazol-5-yl])-methyloxyl-4 call argument compound is not 3-benzyl-57-bis ([Hr-tetrazol-5-yl])-methyloxyl-4 call argument compound is useful for relieving the inhibitory call argument of the call argument is a useful for relieving the inhibitory call argument is a useful for relieving the inhibitory call argument is a serial for relieving the inhibitory call argument sequence is a second and argument argum
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Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
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onen M, Tilgmann C, Lotta T, Kaivola J;
Best Local Similarity 100.0%; Pred. No. 3.7e-06; Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat SERCA 2 inhibitor phospholamban.
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-019625/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6538022-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pollesello P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-1997;
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Query Match

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1 MEKVOYLTRSAIRRAS 16
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ADE45167 standard; protein; 52
                                                                             (first entry)
                                                                           29-JAN-2004
                                                 ADE45167;
RESULT 11
           ADE45167
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Human SERCA\_2 inhibitor phospholamban.

Human; SERCA 2; phospholamban; PLB; Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;

Homo sapiens

cardiant.

note= "S1 binding site residue claimed in claim 1" note= "S1 binding site residue claimed in claim 1" note= "S1 binding site residue claimed in claim 1" note= "S3 binding site residue claimed in claim 1" /note= "S3 binding site residue claimed in claim 1" /note= "S4 binding site residue claimed in claim 1" 'note= "S2 binding site residue claimed in claim 1" 'note= "S3 binding site residue claimed in claim 1" /note= "S4 binding site residue claimed in claim 1" Location/Qualifiers Binding-site Binding-site Binding-site Binding-site Binding-site Binding-site Binding-site Sinding-site US6538022-B1 

25-MAR-2003.

99US-00252063 18-FEB-1999; 97US-00937117

(ORIN ) ORION CORP.

Ovaska M, Tenhunen J, Vidgren J; onen M, Tilgmann C, Lotta T, Kaivola J; Yliperttula-Ikonen M, Pollesello P,

WPI; 2004-019625/02.

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+ -ATPase.

Claim 1; SEQ ID NO 1; 65pp; English

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, ALSTA AFFASSES of the sarco/endoplasmic reticulum ) appearing as ABB45167-ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an SI binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyre, Arg-9 and/or Arg-13; an electronegative moiety associating with an SZ binding site of the phospholamban cytosolic domain when the compound is bound to it, the SZ binding site comprises Arg-14; a hydrophobic moiety associating with an SJ binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety

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associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzyl-5,7-bis ((H+tetrazol-5-yl)-methyloxy)-4-methyl-2H-methyl-2H-benzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2 + -Arpase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is
                                                                                                                                                                                                            human phospholamban.
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Sequence 52 AA;

Gaps .. 0 Length 52; 100.0%; Score 75; DB 8; Length 52 100.0%; Pred. No. 3.7e-06; ive 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches 16; Conserv

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1 MEKVQYLTRSAIRRAS 16

1 MEKVOYLTRSAIRRAS 16

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RESULT 12

AAY71019 standard; protein; 79 AA.

AAY71019;

29-AUG-2000 (first entry)

H6 tagged penetratin-based recombinant protein, H6-(V49A) mutantPLB-ANT.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractilin; inhibitor; cardiac disease; mutant; trantment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedla; H6 tag; hexahistidine. 

Homo sapiens.

Drosophila sp. Synthetic.

Location/Qualifiers Region ćey

/note= "Corresponds to mutant human phospholamban (PLB)

Misc-difference

protein"

 53. .58
 /note= "Corresponds to hexahistidine tag (H6)" "Wild type Val replaced with Ala" note= Region

. 78

Region

/note= "Corresponds to Drosophila antennapedia (ANT)
transport peptide"

WO200025804-A2

11-MAY-2000

99WO-US025692. 02-NOV-1999; 98US-0106718P. 99US-0145883P. 02-NOV-1998; 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

Hoshijima M, Meyer M; Не н, W, Minamisawa S, Silverman GJ; Dillman W, Wang Y, Si Chien K, Scott C,

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCAZA) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCAZA interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the dystunction. The present sequence is the hexahistidine (H6) tagged penetratin-based recombinant protein H6-mutantPLB-ANT, comprising the human mutant (Val 49Ala) PLB protein and Drosophila antennapedia (ANT) expressed in Escherichia coli cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phospholamban, PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hexahistidine tagged penetratin-based recombinant protein, H6-wtPLB-ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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/note= "Corresponds to Drosophila antennapedia (ANT)
transport peptide"
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e= "Corresponds to hexahistidine tag (H6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 75; DB 3; Length 79; 100.0%; Pred. No. 5.8e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
Example 6; Page 56; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71017 standard; protein; 79 AA.
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99US-0145883P.
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nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 79 AA;
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Synthetic.
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Scott C,
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small peptide complexes a martine to the transmitter, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and astrophasmic resticulum (a 2+ Arpase (SERCA2a) within cardiomycoytes. The peptide complexes contraction between PLB and sarcophasmic resticulum (a 2+ Arpase (SERCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against pub protein (contractilin). Penetratin-PLB peptide functions as a contractility and reduces blood pressure. This method is useful for the transmit of cardiac disease e.g. heart failure and myccardial cystunction. The present sequence is the hexahistidine (H6) tagged penetratin-based recombinant protein H6-wPLB-ANT, comprising the wild type human PLB protein and prosophila antennapedia (ANT) transport peptide attached by a hexahistidine tag. This sequence is expressed in Bscherichia coli cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratun; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.
           Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                         The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant marries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 75; DB 3; Length 79; 100.0%; Pred. No. 5.8e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mutant phospholamban (PLB) $16N protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                      Example 6; Page 54-55; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chien K, Dillman W, Scott C, Wang Y, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 79 AA;
                                                                     triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200025804-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Disclosure; Page 49; 56pp; English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum C2 + ATPase (SERCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide complex comprises of transport peptide like penetratin and plb protein (contractilin). Penetratin-PLB peptide functions as a contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the mutation Serl6Asm. This mutant sequence when contractility than the wild type PLB sequence.

Sequence 52 AA;

; 0 0; Gaps Length 52; 96.0%; Score 72; DB 3; Length 52; 93.8%; Pred. No. 1.3e-05; tive 1; Mismatches 0; Indels 1 MEKVQYLTRSAIRRAS 16 1 MEKVOYLTRSAIRRÁN 16 Conservative Local Similarity Les 15; Conserv Query Match datches δ d

ADE45168; RESULT 15 ADE45168

Pig SERCA\_2 inhibitor phospholamban. ADE45168 standard; protein; 52 AA. 29-JAN-2004 (first entry) 

the sarco/endoplasmic reticulum; protein co-ordinate data; Pig; SERCA\_2; phospholamban; PLB; ATPase of cardiant

Sus sp.

US6538022-B1

99US-00252063. 18-FEB-1999; 25-MAR-2003,

97US-00937117. 24-SEP-1997;

(ORIN ) ORION CORP.

Pollesello P, Ovaska M, Tenhunen J, Vidgren J; Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

WPI; 2004-019625/02.

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+ -ATPase.

Claim 1; SEQ ID NO 2; 65pp; English.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, Ca2+ ATPase of the sarco/endoplasmic reticulum ) appearing as ADE45167-

ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr.6, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is abound, the binding site comprises Phe-32 and/or Phe-SC The compound is not 3-benzyl-57-bis ([Hr-tetrazol-5-4)]-methyloxyl-4 methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating the case of phospholamban on cardiac SERCA\_2. The present sequence is a phospholamban. 

Sequence 52 AA;

Gaps ö 96.0%; Score 72; DB 8; Length 52; 93.8%; Pred. No. 1.3e-05; ive 1; Mismatches 0; Indels Local Similarity 93.8 ses 15; Conservative Query Match Matches

1 MEKVQYLTRSAIRRAS 16 1 MDKVOYLTRSAIRRAS 16 ઠે Dp

ADE45169 standard; protein; 52 AA. ADE45169; RESULT 16 ADE45169

29-JAN-2004 (first entry)

Dog SERCA\_2 inhibitor phospholamban.

Dog; SERCA 2; phospholamban; PLB; Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data; cardiant.

Canis sp.

JS6538022-B1.

25-MAR-2003.

99US-00252063. 18-FEB-1999; 97US-00937117. 24-SEP-1997;

(ORIN ) ORION CORP.

Ovaska M, Tenhunen J, Vidgren J; onen M, Tilgmann C, Lotta T, Kaivola J; fliperttula-Ikonen M, Pollesello P,

WPI; 2004-019625/02.

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+ -ATPase.

Claim 1; SEQ ID NO 3; 65pp; English.

The invention relates to a compound which deactivates, and exhibits stiffinity for, a phospholamban (PIB) protein (an inhibitor of SERCA\_2, Ca2+ ATPASE of the sarco/endoplasmic reticulum ) appearing as ADE45167-ADE45173. The compound has a structure containing three of the four angeleis: an electronegative moiety associating with an SI binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative

1 16:13:12 2004

Fri Oct

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moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site comprises Arg-14; a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of mointees Phe-32 and/or Phe-35. The compound is a bound, the binding site of the terazol-5-y1)-methyloxy1-2H-methyl-2H-methyl-2H-methyloxy1-4, methyloxy1-2H-methyl-2H-methyloxy1-4, methyloxy1-4 comproming administering the novel compound to stimulate the Ca 2 + -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phospholamban, PLB, human, sarcoplasmic reticulum Ca 2+ ATPase, SERCA2a, cardiant, cardianyocyte; transport peptide, penetratin, cargo peptide, contractilin; cardiac contractility, inhibitor; cardiac disease, mutant, treatment; heart failure; myocardial dysfunction; recombinant protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Corresponds to denatured human immunodeficiency virus (HIV) TAT protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penetratin-based recombinant phospholamban peptide, TAT-mutant PLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoshijima M, Meyer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.0%; Score 72; DB 8; Length 52; 93.8%; Pred. No. 1.3e-05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Ser replaced with Glu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY71014 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silverman GJ;
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99US-0145883P.
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Best Local Similarity
Local Similarity
Local 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-365393/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV; TAT protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 phospholamban.
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27-JUL-1999;
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Scott C,
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small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum (a 2+ Arpase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a contractility and reduces blood pressure. This method is useful for the trachment of cardiac disease e.g. heart failure and myocardial cyptide TAT-mutant PLB, comprising the amino terminal end of human PLB mutant (Ser31Glu) protein, attached to the 3' end of denatured human pub immunodeficiency virus (HIV), TAT protein. Penetratin is a class of peptides, with translocating protein, penetratin is a class of hydrophilic compounds across the plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardlomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia.
                                                                                                                   discloses a method for the treatment of heart failure, using

    .20
/note= "Corresponds to mutant human phospholamban (PLB)
amino terminal peptide"

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/note= "Corresponds to Drosophila antennapedia (ANT)
transport peptide"
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71013 standard; peptide; 36 AA.
                                                             Example 5; Page 53; 56pp; English.
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99US-0145883P.
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   triphosphatase.
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Best Local S
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AAY71013
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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ Arpase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the dysfunction. The present sequence is the penetratin-based recombinant optide, mutant PLB-ANT, comprising the amino terminal end of human PLB mutant (SerI6Glu) protein, attached to the S' end of the Drosophila antennapedia (ANT) transport peptide. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the plasma membrane
                                                                  Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.7%; Score 71; DB 3; Length 36; 100.0%; Pred. No. 1.3e-05; ... tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human phospholamban pseudophosphorylation mutant S16E PLB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                       Example 5; Page 53; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB79404 standard; peptide; 52 AA.
 Silverman GJ
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Matches 15; Conservative
                                   WPI; 2000-365393/31.
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(HOSH/) HOSHIJMA M.
(ROSS/) ROSS J.
 Wang Y,
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                                                                                                                        triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 AA;
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 Scott C,
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Delivering a dose of a gene expression cassette in a fluid selectively to heart for sustained expression, useful for improving or enhancing cardiac function, by employing a viral vector together with a vascular permeablizing agent.
                                                                                                                                                        The invention relates to delivering a therapeutic dose of a gene expression cassette in a fluid selectively to heart for sustained expression, comprising employing a viral vector together with a vascular permabbilising agent. The method is useful for gene therapy delivering genes for improving or enhancing cardiac function, particularly in hamster models of heart disease. The present sequence is that of a pseudophosphorylation mutant of phospholamban (SIGEPLB). This point mutant is among a number of dominant negative mutants identified and characterised in WOO0/25804 and used in the method of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicken; SERCA_2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
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onen M, Tilgmann C, Lotta T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chicken SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 7; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE45173 standard; protein; 52 AA.
                                                                                                                         Example 6; Fig 1; 12pp; English.
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WPI; 2002-361185/39.
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                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                           Sequence 52 AA;
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of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative moiety associating with an $2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the $2 binding site comprises Arg-14; a hydrophobic moiety associating with an $3 binding site of the phospholamban cytosolic domain when the compound; the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or bhen the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is not 3-benzopxan-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2 + -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ Arpase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; andiac contractility; inhibitor; cardiac disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H6 tagged penetratin-based recombinant protein, H6-(S16E)mutantPLB-ANT.
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                                                                                                                                                                                                                                                                                                                                        0; Gaps
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/note= "Corresponds to Drosophila antennapedia (ANT)
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                                                                                                                                                                                                                                                                                                      94.7%; Score 71; DB 8; Length 52; 87.5%; Pred. No. 2e-05; 1rde 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY71018 standard; protein; 79 AA.
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                                                                                                                                                                                                                                                                                                                                                                      1 MEKVOYLTRSAIRRAS 16
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                                                                                                                                                                                                                                                                       Sequence 52 AA;
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                                                                                                                                                                                                                                       phospholamban.
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Synthetic.
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Scott C,
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phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomycytes. The peptide complexes of transport peptide like penetratin and cargo peptide complexes of transport peptide like penetratin and cargo peptide complexe comprises of transport peptide like penetratin and PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the hexahistidine (H6) tagged penetratin-based recombinant protein H6-mutantPLB-ANT, comprising the human mutant (SerlGGlu) PLB protein and Drosophila antennapedia (ANT) transport peptide attached by a hexahistidine tag. This sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
                              Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                      patent discloses a method for the treatment of heart failure, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiant, cardiomyocyte, transport peptide, penetratin; cargo peptide, contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 79;
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                                                                                                                      Example 6; Page 55; 56pp; English.
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WPI; 2000-365393/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 79 AA;
                                                                                      triphosphatase.
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27-JUL-1999;
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Scott C,
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WPI; 2000-365393/31.

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Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enthancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Disclosure; Page 48-49; 56pp; English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPASE (SERCA2a) within cardiomycoyres. The peptide complex comprises of transport peptide like penetratin and PLB protein (contractilin). Penetratin-PLB peptide like penetratin and pub protein (contractilin) Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising a sense mutation Argiddlu. This mutant sequence when contractility than the wild type PLB sequence

Sequence 52 AA;

ö Gaps ô 93.3%; Score 70; DB 3; Length 52; 93.8%; Pred. No. 3e-05; live 0; Mismatches 1; Indels Local Similarity 93,8 tes 15; Conservative Query Match Best Loca Matches

1 MEKVOYLTRSAIRRAS 16 ò

1 MEKVQYLTRSAIREAS 16 g

RESULT 23

AAY71004 standard; protein; 52 AA. AAY71004;

(first entry) 29-AUG-2000

Human mutant phospholamban (PLB) E2A protein.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant, cardiamycocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.

Homo sapiens Synthetic. Location/Qualifiers Misc-difference 2

/note= "Wild type Glu replaced with Ala"

WO200025804-A2

11-MAY-2000

99WO-US025692 02-NOV-1999; 98US-0106718P 99US-0145883P 02-NOV-1998; 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

Hoshijima M, не н, Dillman W, Minamisawa S, Wang Y, Silverman GJ; Chien K, Scott C, 

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Disclosure, Page 48; 56pp; English.

small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2 + ATPase (SERCA2a) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the mutation diuzala. This mitant sequence when contractility than the wild type PLB sequence patent discloses a method for the treatment of heart failure, using

Sequence 52 AA;

Gaps ; 0 Length 52; 1; Indels 92.0%; Score 69; DB 3; L 93.8%; Pred. No. 4.6e-05; live 0; Mismatches 1; Local Similarity 93.8 es 15; Conservative Query Match Matches

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1 MAKVOYLTRSAIRRAS 16 1 MEKVOYLTRSAIRRAS

g

à

16

RESULT 24

AAY71007 standard; protein; 52 AA.

AAY71007;

(first entry) 29-AUG-2000

Human mutant phospholamban (PLB) K3E/R14E protein.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardianycorte; transport peptide; penetratuin; cardiac operactility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant. 

sapiens.

Synthetic.

note= "Wild type Lys replaced with Glu" /note= "Wild type Arg replaced with Glu" Location/Qualifiers Misc-difference 14 Misc-difference

WO200025804-A2

11-MAY-2000.

99WO-US025692 02-NOV-1999; 98US-0106718P. 02-NOV-1998; 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

Meyer M; He H, Hoshijima M, Minamisawa S, Dillman W, Minamisawa Wang Y, Silverman GJ; Chien K, Scott C. Scott

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine riphosphatase.

Disclosure; Page 49; 56pp; English.

small peptide complexes and recombinant proteins, that induces the phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2.4 ATPase (SERCA2A) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, mative PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and mycardial dysfunction. The present amino acid sequence is the human mutant PLB protein. Comprising the double mutaction hysaldu and Argisclu. This mutant sequence, when overexpressed in the transformed cardiomycytes, shows increased contractility than the wild type PLB sequence The patent discloses a method for the treatment of heart failure, using

Sequence 52 AA;

Gaps ö 88.0%; Score 66; DB 3; Length 52; 87.5%; Pred. No. 0.00016; 1; Mismatches 1; Indels 1 MEKVOYLTRSAIRRAS 16 1 MEEVQYLTRSAIREAS 16 Local Similarity 87.5 les 14; Conservative Query Match Matches ö g

ADC87928 standard; protein; 116 AA. (first entry) 01-JAN-2004 ADC87928;

Antifungal protein; ribosomal protein; FCWP1; AlyAFP; Ribosomal protein similar to FCWP1 #144. 

plant fungal infection; Alternaria; Ascochyta; Bótrytis; Cercospora; Colletotrichum; Diplodia; Fusarium; Gaeumanomyces; Helminthosporium; Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma; Phymatotrichum; Phytophthora; Plasmopara; Podosphaera; Puccinia; Puthium; Pyrenophora; Plasmopara; Podosphaera; Puccinia; Puthium; Syrenophora; Perinia; Puthium; Raizotconia; Scerotium; Sclerotinia; Septoria; Thielaviopsis; Venturia; Verticillium.

US6573361-B1.

03-JUN-2003.

07-DEC-2000; 2000US-00732210.

99US-0169340P. 07-DEC-1999; 07-DEC-1999; (MONS ) MONSANTO TECHNOLOGY LLC.

Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS; WPI; 2003-754558/71. Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful for controlling fungal infections in plants.

Example 21; SEQ ID NO 181; 27pp; English.

The invention relates to an isolated antifungal ribosomal protein from

(e.g. Wycoghuereria inguentals), Nectica (Nectical Coccas), Phoma Detae), Phymatotrichum (e.g. Phymatotrichum (e.g. Phymatotrichum (e.g. Phymatotrichum omnivorum), Phytophthora parasitica, Phytophthora cactorum, Phytophthora parasitica, Phytophthora cactorum, Coccatorum, Phytophthora parasitica, Phytophthora (e.g. Phytophthora parasitica, Phytophthora (e.g. Phytophthora parasitica, Phytophthora (e.g. Phytophthora parasitica, Phytophthora (e.g. Phytophthora (e.g. Phytophthora (e.g. Phytophthora (e.g. Pragnapara viticola), Podosphaera (e.g. procinia graminis f.sp. tritici, Puccinia asparasi, Puccinia graminis f.sp. tritici, Puccinia asparasi, Phytophthora (e.g. Phytophthora (e.g. Pytriularia (e.g. Scerotium Polfsii), Sclerotinia (e.g. Scerotium Phaeosphaeria (e.g. Septoria glycinia (e.g. Septoria glycinia (e.g. Septoria diginia parasionia), Uncinula (e.g. Uncinula necator), Venturia nodorum, Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium albo-atrum). Mutations in the proteolytic consensus contained within FCMP1 provides improved stability of its sequences contained within FCMP1 provides improved stability of its antifungal activity. Also disclosed are ribosomal proteins with similar consensus proteins similar to FCMP1, which may act as antifungal staticillium delications in the proteolytic consensus antifungal proteins The present sequence represents one of the ribosomal proteins similar to FCMP1 (e.g. Proteins similar to FCMP1) which may act as antifungal activity. New disclosed are ribosomal proteins with similar consensus contained within FCMP1 provides tepresents one of the ribosomal proteins similar to FCMP1, which may act as antifungal series similar to FCMP1, which may act as antifungal activity. New disclosed are ribosomal proteins with similar consensus contained within FCMP1) and molecular weight (<2000a) to F signal peptide of the antifungal protein AlyAFP from Alyssum and PCWP1, encoded by the nucleic acid appearing as ADC87758. The PCWP1 proteins are useful for controlling fungal infections in plants, such as those caused by Alternaria (e.g. Alternaria brassicola, Alternaria solani), Ascochyta (e.g. Ascochyta pisi), Botrytis (e.g. Botrytis cinerea), Carcospora (e.g. Ascochyta pisi), Botrytis (e.g. Botrytis cinerea), Collectotrichum (e.g. Collectotrichum indemuthianum), Diplodia (e.g. Diplodia maydis), Pusarium (e.g. Fusarium mivale, Pusarium oxysporum, Fusarium graminearum, Pusarium culmorum, Fusarium solani, Fusarium moniliforme, Fusarium roseum), Gaeumanomyces (e.g. Macrophomina phaseolina, Maganaporthe grisea), Mycosphaerella (e.g. Mycosphaerella figiensis), Nectria heamatococa), fusarium culmorum, FCWP1. Also included is a fusion protein between the segdata.uspto.gov/seguence.html?DocID=6573361Bl.

Sequence 116 AA; 

ö 0; Gaps Score 41; DB 7; Length 116; Pred. No. 14; 3; Indels Mismatches 54.7%; Scc. 46.7%; Pred 5; 1 Query Match
Best Local Similarity 46...
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sequence 9, Application US/09252063
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sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 10 Sequence 
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APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Piero
APPLICANT: Tenhunen, Jukka
APPLICANT: Tenhunen, Jukka
APPLICANT: Tenhunen, Jukka
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Timo
APPLICANT: Lotta, Timo
TITLE OF INVENITION: Ca-AIPESE (Phospholamban Inhibitors)
FILE REFERENCE: 1102.025001
CURRENT APPLICATION NUMBER: 08/09/252,063
CURRENT FILING DATE: 1999-02-18
ERRLIER APPLICATION NUMBER: 08/337,117
ERRLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SSP ID NO 1
LENGTH: 52
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US-09-252-063-9
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100.0%; Score 75; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
ALIGNMENTS
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KESULT 4

US-09-252-063-5
; Sequence 5, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: POLISEALIO, Piero
; APPLICANT: Pollseallo, Piero
; APPLICANT: Tanhunen, Jukka
; APPLICANT: Tanhunen, Jukka
; APPLICANT: Tilgmann, Carola
; APPLICANT: Raivola, Juha
; TILLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; TILLE OF INVENTION: Ca-APPLED
; TILLE OF INVENTION: NUMBER: US/09/252, 063
; CURRENT FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOTTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 5
; LEWARTH: DATE: DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
APPLICANT: Tiperttula-Ikonen, Marjo
APPLICANT: Tiperttula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Cofte, Timo
APPLICANT: Cofte, Timo
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Ca-ArPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
GURRENT APPLICATION NUMBER: 08/9252,063
GURRENT APPLICATION NUMBER: 08/937,117
EARLIER PILING DATE: 1999-02-18
FERENET PILING DATE: 1999-02-18
FERENTER PILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
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Query Match
100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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US-09-252-063-4
; Sequence 4, Application US/09252063
. Datent No. 6538022
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LENGTH: 52
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
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; ORGANISM: Rattus sp.
US-09-252-063-5
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us-09-830-779-8.rai

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| PATENT NO. 9.2.0.0.c.
| GENERAL INFORMATION:
| APPLICANT: POILGEGELIO, Piero
| APPLICANT: Poilgeello, Piero
| APPLICANT: Poilgeello, Piero
| APPLICANT: Tahunen, Jukka
| APPLICANT: Yilpertula-Ikonen, Marjo
| APPLICANT: Yilpertula-Ikonen, Marjo
| APPLICANT: Tilgmann, Carola
| APPLICANT: Tilgmann, Carola
| APPLICANT: Tilgmann, Carola
| APPLICANT: Lotta, Timo
| APPLICANT: Compounds for Deactivating Phospholamban Function on
| TITLE OF INVENTION: Ca-Argae (Phospholamban Inhibitors)
| TITLE OF INVENTION: Ca-Argae (Phospholamban Inhibitors)
| TITLE OF INVENTION NUMBER: US/09/252,063
| CURRENT FILING DATE: 1997-09-24
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: Patentin Ver: 2.0
| LENGTH: 52
| TYPE: RT
| CRANISM: Sus sp.
| US-09-252-063-2
| US-09-253-063-2

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FAUCHAT: Pollesello, Piero

APPLICANT: Pollesello, Martki

APPLICANT: Tenhunen, Jukka

APPLICANT: Tenhunen, Jukka

APPLICANT: Tilgann, Carola

APPLICANT: Tilgann, Carola

APPLICANT: Tilgann, Carola

APPLICANT: Tilgann, Carola

APPLICANT: APPLICANT: Compounds for Deactivating Phospholamban Function on

TITLE OF INVENTION: Cappounds for Deactivating Phospholamban

TITLE OF INVENTION: Cappounds for Deactivating 
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100.0%; Score 75; DB 4; Length 52; 100.0%; Pred. No. 3e-07; tive 0; Mismatches 0; Indels
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; Sequence 2, Application US/09252063
; Patent No. 6538022
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Patent No. 6538022
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Query Match
Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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US-09-252-063-3
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LENGTH: 52
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US-09-252-063-6

Sequence 6, Application US/09252063

Patent No. 653802

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Piero
APPLICANT: Tenhunen, Jukka
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Arivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250016

CURRENT APPLICATION NUMBER: US/09/252,063

CURRENT APLICATION NUMBER: US/09/252,063

EARLIER PILING DATE: 1999-02-18

BARLIER PILING DATE: 1999-09-24

NUMBER OF SEQUENCE: 1102.0550016

NUMBER OF SEQUENCE: 1102.0550016

MUMBER OF SEQUENCE: 1102.055016
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                                                                                                                                                        0; Gaps
                                                    Query Match
100.0%; Score 75, DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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Patent No. 6540996

GREBEAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Zwaal, Richard
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 1999-04-15
SROUPH THING DATE: 1999-04-15
                                                                                                                                                                                                                                                      1 MEKVOYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                      1 MEKVQYLTRSAIRRAS 16
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SEQ ID NO 6
LENGTH: 52
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US-09-549-872B-15
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US-09-549-872B-15
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us-09-830-779-8.rai

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APPLICANT: Pollecello, Piero
APPLICANT: Pollecello, Marti
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Juka
APPLICANT: Vidgren, Juka
APPLICANT: Asivola, Juha
APPLICANT: Cotta, Timo
APPLICANT: Cotta, Timo
APPLICANT: Compounds for Deactivating Phospholamban Function on
TITLE OF INVENTION: Ca-Appase (Phospholamban Inhibitors)
TITLE OF INVENTION: Ca-Appase (Phospholamban Inhibitors)
FILE REPERROR: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT APPLICATION NUMBER: 08/937,117
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER PLING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: S.2
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                                                                                                 Gaps
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Query Match 96.0%; Score 72; DB 4; Length 52; Best Local Similarity 93.0%; Pred. No. 1.1e-06; Matches 15; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-549-872B-14
| Sequence 14, Application US/09549872B
| Patent No. 6540996
| GENERAL INFORMATION:
| APPLICANT: Zwaal, Richard
| APPLICANT: Groenen, Jose
| APPLICANT: Begaert, Thichery
| TITLE OF INVENITION: COMPOUND SCREENING METHODS
| PILE REFERENCE: D00590/70000 (JRV/RE)
| CURRENT APPLICATION NUMBER: US/09/549,872B
| CURRENT FILING DATE: 1999-04-14
| PRIOR FILING DATE: 1999-04-15
| RIGHT FILING D
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                                                                                                                                                                               1 MEKVOYLTRSAIRRAS 16
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Matches 15, Conservative
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; ORGANISM: Gallus sp.
US-09-252-063-7
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Sequence 18000, Application US/09252991A

Patenta INCORATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL MACC J. Rubenfield et al.
TITLE OF INVENTION:
FILE REPERENCE:
107196.136
GURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRICK PALICATION NUMBER: US 60/074,788
FRICK PALICATION NUMBER: US 60/074,788
FRICK PALICATION NUMBER: US 60/094,190
FRICK APPLICATION NUMBER: US 60/094,190
FRICK PALING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18600
LENGTH: 631
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APPLICANT: Bunkers, Greg J.

APPLICANT: Liang, Jihong

APPLICANT: Liang, Jihong

APPLICANT: Mitaanck, Cindy A.

APPLICANT: Seale, Jeffrey W.

APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: ALL: fungal Proteins and Methods for Their Use

FILE REFERENCE: 38-21(1505)8

CURRENT APPLICATION NUMBER: US/09/732,210

CURRENT APPLICATION NUMBER: US 60/169,513

PRIOR PILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO 181

FUNDER OF SEQ ID NOS: 1753
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Query Match 94.7%; Score 71; DB 4; Length 52; Best Local Similarity 87.5%; Pred. No. 1.7e-06; Matches 14; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                       ; Sequence 181, Application US/09732210; Patent No. 6573361; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                  1 MEKVOYLTRSAIRRAS 16
                                                                                                                                                   1 MEKVOYLTRSAIRRA 15
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Matches 7; Conservative
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US-09-252-991A-18000
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Sequence 24791, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TOTALE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/074,788
PRIOR APPLICATION NUMBER: US/074,788
PRIOR PELING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142

LENGTH: 765
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48.0%; Score 36; DB 4; Length 686;
Best Local Similarity 77.8%; Pred, No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
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48.0%; Score 36, DB 4; Length 765;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 3; Indels
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US-08-588-983-18
Sequence 18' Application US/08588983
Fatent No. 5854067
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: For Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: Houston
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/588,983 FILING DATE: Concurrently herewith
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24791
                                                                                                          TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19332
        1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502 EQVRWLDREELRRA 515
, PRIOR FILING DATE: 1998-07-2
NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19332
LENGTH: 686
; TYPE: PRT
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US-09-252-991A-24791
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US-09-1262-991A-19332
US-09-1262-991A-19332
Sequence 19332, Application US/09252991A
Patent No. 6551795
GENERAL INFERMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
PILE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION:
PILE REPERRICE:
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
                                                               Sequence 7319, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Execton et. al
APPLICANT: Gary Execton et. al
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: WUMBER: 2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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Factor No. 6610836
GENERAL INFORMATION
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WHERE: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
FRICK REPLICATION NUMBER: US 60/117,747
FRICK POS SEQ ID NOS: 14342
SEQ ID NO 11011
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Pred. No. 15;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Klebsiella pneumoniae US-09-489-039A-11071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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51 KPQHLTRSGMRK 62
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US-09-489-039A-11071
                         RESULT 13
US-09-489-039A-7319
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Sequence 6395, Application US/09134000C
Patent No. 6617156
GENERAL INPORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: MUCHENCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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US-09-134-001C-5136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 EKVDFLTKEIERRIT 196
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Best Local Similarity 46.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 53.8
Matches 7; Conservative
                                     RESULT 19
US-09-252-991A-28362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 48.0%; Score 36; DB 2; Length 924; Best Local Similarity 61.5%; Pred. No. 1.8e+02; Matches 8; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/08588976;
Patent No. 5891717;
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTION: Inhibiting Haxokinase;
MUMBER OP SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALOLGA, White & Durkee
STREET: P.O. Box 4433
COTTY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER ERABBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC COMPATIBLE
COMPUTER: IBM FC COMPATIBLE
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,976
FILING DATE: Concurrently herewith
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fussey, Shelley P.M.
REGISTATION NUMBER: 39,458
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
48.0%; Score 36; DB 2; I
Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 4
                                                                          UTSD:424/FUS
NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REPRENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
TYPE
                                                                                                                                                                                                    TELEX: n/a
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     638 QDVVYLLREAIRR 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     638 ODVVYLLREAIRR 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EKVOYLTRSAIRR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EKVOYLTRSAIRR 14
                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-588-983-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-588-976-18
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US-08-588-976-18
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US-09-134-001C-5136

Sequence 5136, Application US/09134001C

Sequence 5136, Application US/09134001C

Sequence 5136, Application US/09134001C

SEMENTAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEPLEMENT OF TOWN THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR PLING DATE: 1997-11-08

PRIOR PLING DATE: 1997-11-08

PRIOR FILING DATE: 1997-06-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO. 5136

LINGTH: 211
                                                                                                         Patent No. 6551795
Sequence 28362, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPBUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLICATION NUMBER: US 60/074,768
PRIOR PLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28362
LENGTH: 210
ATTORNEY/AGENT INFORMATION:
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Patent No. 6635750

GENERAL INFORMATION:

APPLICANT: COVIE, Anthony J.

APPLICANT: Braser, Christopher C.

APPLICANT: Manning, Stephen

TITLE OF INVENTION: E-Maily and Uses Thereof

TITLE REFERENCE: 5800-149

CURRENT APPLICATION NUMBER: US/09/620,461

CURRENT PILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 14

LINGTH: 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Coyle, Anthony J.
APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 35800/336924
CURRENT APPLICATION NUMBER: US/09/910,174B
CURRENT APPLICATION NUMBER: US/09/910,174B
FRIOR APPLICATION NUMBER: US 09/620,461
PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 357
                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                 Query Match
46.7%; Score 35; DB 4; Length 216;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 4; Indels
CURRENT APPLICATION NUMBER: US/09/134,000C;
CURRENT FILING DATE: 1998-08-13;
PRIOR APPLICATION NUMBER: US 60/055,778;
PRIOR FILING DATE: 1997-08-15;
NUMBER OF SEQ ID NOS: 6812;
SEQ ID NO 6395;
LENGTH: 216;
TYPE: PRT
CREANIEM: ENTEROCOCCUS faecalis
US-09-134-000C-6395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-910-174B-14
; Sequence 14, Application US/09910174B
; Patent No. 6630575
                                                                                                                                                                                                                                                                                                                                                                                                                                161 QYINRETLRRVS 172
                                                                                                                                                                                                                                                                                                                                                                                                   5 QYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-910-174B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 KKIQYLTR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CAGANISM: Homo sapiens
US-09-620-461-14
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Sequence 2, Application US/09277262

| Sequence 2, Application US/09277262
| Patent No. 6395482
| GeneRal INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: GASOS, JOSEPH A
| TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
| TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
| TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
| TITLE OF INVENTION: METHOD OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
| TITLE OF INVENTION: METHOD OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
| TITLE OF INVENTION: US/09/277,262
| TITLE OF INVENTION: US/09/277,262
| CURRENT APPLICATION NUMBER: 09/229,530
| EARLIER PILING DATE: 1999-01-13
| NUMBER OF SEQ ID NOS: 9
| SEQ ID NO 2 |
| LENGTH: 516
| TYPE: PRT
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-09-277-262-2
                                                                                                                                                                                                                                                                                                                                                    US-09-277-262-4

| Sequence 4, Application US/09277262 |
| Sequence 4, Application US/09277262 |
| Sequence 4, Application US/09277262 |
| Sequence 5, Application US/09277262 |
| GENERAL INFORMATION: APPLICANT: Karayiorgou, Maria |
| APPLICANT: Karayiorgou, Maria |
| APPLICANT: GASOS, JOSEPH BA |
| TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE |
| TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED |
| TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED |
| TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED |
| TITLE OF INVENTION: 1999-03-26 |
| FILE REFERENCE: 600-1-223 GTP |
| CURRENT APPLICATION NUMBER: US/09/277,262 |
| EARLIER PILING DATE: 1999-03-26 |
| EARLIER PILING DATE: 1999-01-13 |
| NUMBER OF SEQ ID NOS: 9 |
| SEQ ID NO 4 |
| LENGTH: 497 |
| LENGTH: 497
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                                                                             0; Gaps
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Query Match
46.7%; Score 35; DB 4; Length 357;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
46.7%; Score 35; DB 4; Length 516;
Best Local Similarity 43.8%; Pred, No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 MEVLPYLSRRALENSS 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471 MEVLPÝLSRRÁLENSS 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus
US-09-277-262-4
                                                                                                                                                                                                                313 KKIOYLTR 320
                                                                                                                                              2 EKVOYLTR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-277-262-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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Search completed: October 1, 2004, 12:21:10 Job time : 19 secs

us-09-830-779-8.rai

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October 1, 2004, 12:18:23 ; Search time 63.4 Seconds (without alignments) 81.211 Million cell updates/sec
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17: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp;*

18: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp;*

18: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp;*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       US-09-830-779-8
75
1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Sequence:
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                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Sequence 8, Appli | 10,              | 2               | 4               | ທ               | Sequence 15, Appl | Sequence 478, App  | Sequence 1, Appli | 'n              | Sequence 17, Appl | 19,              | 3,              | 14,              | Sequence 5. Appli |
|-------------------------------|-------------------|------------------|-----------------|-----------------|-----------------|-------------------|--------------------|-------------------|-----------------|-------------------|------------------|-----------------|------------------|-------------------|
| SUMMARIES                     | US-10-705-791-8   | US-10-705-791-10 | US-09-954-571-2 | US-09-954-571-4 | US-09-954-571-5 | US-10-371-101-15  | US-10-408-765A-478 | US-10-705-791-1   | US-10-705-791-2 | US-10-705-791-17  | US-10-705-791-19 | US-09-954-571-3 | US-10-371-101-14 | US-10-705-791-5   |
| DB                            | 16                | 7                | 12              | 12              | 12              | 14                | 16                 | 16                | 16              | 16                | 16               | 12              | 14               | 16                |
| %<br>Query<br>Match Length DB | 16.               | 9 6              | 52              | 52              | 52              | 52                | 52                 | 52                | 52              | 79                | 79               | 52              | 52               | 52                |
| %<br>Query<br>Match           | 100.0             | 100.0            | 100.0           | 100.0           | 100.0           | 100.0             | 100.0              | 100.0             | 100.0           | 100.0             | 100.0            | 96.0            | 96.0             | 96.0              |
| Score                         | 75                | 75               | 75              | 75              | 75              | 75                | 75                 | 75                | 75              | 75                | 75               | 72              | 72               | 72                |
| Result<br>No.                 | 1                 | m                | 4               | 'n              | 9               | 7                 | æ                  | თ                 | 10              | 11                | 12               | 13              | 14               | 15                |

| - ααταστημομερον «φοφιρια Φονο ωφιρον «ο σε «αυσστασσσσσσσσσσσσσσσσσσσσσσσσσσσσσσσσσ | 4 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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Page 2

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Sequence 10, Application US/10705791

Fublication No. US20040121942A1

GENERAL INFORMATION:

APPLICANT: The Regents of the University of California

APPLICANT: Chien, Kenneth

APPLICANT: Dillmann, Wolfgang

APPLICANT: He, Huaping

APPLICANT: He, Huaping

APPLICANT: He, Huaping

APPLICANT: He, Huaping

APPLICANT: Goott, Christopher

APPLICANT: Wancy, Yibin

APPLICANT: W
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
CHERENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR PLING DATE: 1996-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR PLING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENT OF SEQ ID NOS: 19
SOFTWARE: SEC ID NOS: 19
LENGTH: 35
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100.0%; Pred. No. 1.2e-06;
tive 0; Mismatches 0;
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PRIOR FILING DATE: 1998-11-02
PRIOR PLING DATE: 1998-11-02
PRIOR PLING DATE: 1999-11-02
NUMBER: PCT/US99/25692
NUMBER: PCT/US99/25692
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Sequence 2, Application US/09954571
Publication No. US20202032167A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 19
SOFWARE: Patentin version 3.2
SEQ ID NO 36
LENGTH: 36
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Best Local Similarity 100.0
Matches 16; Conservative
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CORGANISM: Homo sapiens
US-10-705-791-10
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-705-791-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 16; Conserv
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US-10-705-791-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hat Haping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Moyer, Markus
APPLICANT: Moyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Salverman, Gergg J.
ITILE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
ITILE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
FILLE REFERENCE: 6627-Teagol25
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: D6/106,718
PRIOR FILLING DATE: 1998-11-02
PRIOR FILLING DATE: 1998-11-02
PRIOR FILLING DATE: 1998-11-02
PRIOR FILLING DATE: 1999-11-02
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 19
LENGTH: 16
LENGTH: 16
                                    Sequence 147002,
Sequence 1011, A
Sequence 1011, A
Sequence 442, App
Sequence 442, App
Sequence 742, App
Sequence 7111, A
Sequence 57201, A
Sequence 164, App
Sequence 2255, App
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100.0%; Score 75; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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Sequence 11, Application US/10705791
Sequence 11, Application US/10705791
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Dillmann, Wolfgang
           US-10-424-599-152503
US-10-437-963-14702
US-10-437-963-103091
US-10-372-876-442
US-10-097-065-442
US-10-12-944-464
US-10-282-1228-71171
US-10-093-463-16
US-10-1034-463-16
US-10-093-463-167
US-10-093-463-167
US-10-093-463-167
US-10-093-463-168
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He, Huaping
Hoshijima, Masahiko
Meyer, Markus
Scott, Christopher
Wang, Yibin
Silverman, Gregg J.
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US-10-705-791-8
                RESULT 1
US-10-705-791-8
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APPLICANT:
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                   APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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US-09-954-571-5
; Sequence 5, Application US/09954571
; PUDLICATION No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Office, Kenneth R
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Ross, John
; APPLICANT: Reas, John
; APPLICANT: Reas, John
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION UNMBER: 60/231,821
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ross, John
APPLICANT: Ross, John
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT PILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 5
LENGTH: 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 75; DB 12; Length 52; Best Local Similarity 100.0%; Pred. No. 1.9e-06; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chien, Kenneth R
APPLICANT: Chien, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Rose, John
APPLICANT: Rose, John
APPLICANT: IRGA, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFREENCE: 6627-PA0123
CURRENT APPLICATION WOBER: US/09/954,571
CURRENT APPLICATION WUMBER: 06/0231,821
PRIOR APPLICATION WUMBER: 60/231,821
PRIOR PILING DATE: 200-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08954571 Publication No. US20020032167A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MEKVQYLTRSAIRRAS 16
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                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-954-571-2
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US-09-954-571-4
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US-09-954-571-4
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| Sequence 478, Application US/10408765A
| Publication No. US20040101874A1
| GENERAL INPORMATION:
| APPLICANT: Fahy, Eoin D.
| APPLICANT: Taylor, Steven W.
| APPLICANT: Taylor, Steven W.
| APPLICANT: Gibson, Bradford W.
| APPLICANT: Gibson, Dane E.
| TILE OF INVENTION: TAKEBTS FOR THERAPEUTIC INTERVENTION TILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROFEOME FILE REFERENCE: 66008465
| CURRENT APPLICATION NUMBER: US/10/408,765A
| NUMBER OF SEQ ID NOS: 3077
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                             Query Match 100.0%; Score 75; DB 12; Length 52; Best Local Similarity 100.0%; Pred. No. 1.9e-06; Matches 16; Conservative 0; Mismatches 0; Indels
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GRERAL INFORMATION:
APPLICANT: Greenen, Jose
APPLICANT: Greenen, Jose
APPLICANT: Begeart, Thierry
TILLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035.US
CURRENT APPLICATION NUMBER: US/10/311,101
CURRENT APPLICATION NUMBER: US/10/311,101
PRIOR FILING DATE: 1999-04-15
PRIOR PAPLICATION NUMBER: US 60/129,596
PRIOR PILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-11
PRIOR PILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: O9/549,872
PRIOR FILING DATE: 2000-04-14
SOFTWARE: PATENTION UNUMER: O9/549,872
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN UNIVER: OF SEQ ID NOS: 39
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/10371101
Publication No. US20030149995A1
GENERAL INFORMATION:
                                                                                                             TYPE: PRT; ORGANISM: Oryctolagus cuniculus US-09-954-571-5
, NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
: SEQ ID NO 5
; LENGTH: 52
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CRGANISM: Homo sapiens
US-10-371-101-15
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APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: Minamisawa, Susanne
APPLICANT: Minamisawa, Susanne
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Mang, Yibin
APPLICANT: Mang, Yibin
APPLICANT: Wang, Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 52;
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; Publication No. US20040121942A1
; GENERAL INPORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT PELICATION NUMBER: US/11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 19
SOFWARE: PATENTIN VERBION 3.2
LENGTH: 52
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Publication No. US20040121942A1
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GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 16, Conservative
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Best Local Similarity 100.0
Matches 16, Conservative
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US-10-705-791-17
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/ ORGANISM: Homo sapiens
US-10-705-791-2
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US-10-705-791-17
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US-10-705-791-19
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APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Maskus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gragg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
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Hoshljima, Masahiko
Meyer, Markus
Scott, Christopher
Wang, Yibin
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                                    LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                           US-10-408-765A-478
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US-10-705-791-2
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          ; SEQ ID NO 478
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LENGTH: 52
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APPLICANT: SILVEYMENT Gregg J.

TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REPERENCE: 6627-289025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: 607106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTI Version 3.2
SOFTWARE: PATENTI Version 3.2
LENGTH: 52
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TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFREENCE: DO0590.70015.US
FULRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003.02.21
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR PELLING DATE: 1999-04-15
PRIOR PELLING DATE: 1999-04-15
PRIOR PELLING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR PELLING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET: 2.0
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Best Local Similarity 93.88
Matches 15; Conservative
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US-10-705-791-5
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US-10-705-791-13
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TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: 60/106,718
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR APPLICATION NUMBER: PCT/US99/25692
RIOR APPLICATION NUMBER: PCT/US99/25692
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VERSION 3.2
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; Bublication No. US20020032167A1
; GENERAL INVORMATION:
; APPLICANT: Chien, Kenneth R
; APPLICANT: Hoehijima, Maaahiko
; APPLICANT: Ross, John
; PILLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR PILLING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOCTWARRE: Patentin Version 3.2
; LENGTH: 52
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US-10-371-101-14
US-10-371-101-14
i Sequence 14, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Begaert, Thierry
                               He, Huaping
Hoshijima, Masahiko
Meyer, Markus
Scott, Christopher
Wang, Yibin
        Minamisawa, Susanne
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US-10-705-791-19
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; ORGANISM: Canis familiaris
US-09-954-571-3
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Matches 15; Conservative
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LENGTH: 79
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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Publication No. US20040121942A1

GENERAL INFORMATION:

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1 MEKVOYLTRSAIRRA 15

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TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT TITLE OF INVENTION: OF CARDIAC DISEASE FILE REFERENCE: 6627-PA9035 CURRENT APPLICATION WIMBER: US/10/705,791 CURRENT PAPLICATION WIMBER: US/10/705,791 CURRENT FILING DATE: 2003-11-10 PRIOR PILING DATE: 1998-11-02 PRIOR FILING DATE: 1998-11-02 PRIOR FILING DATE: 1999-11-02 PRIOR FILING DATE: 1999-11-02 SOFTWARE: DEACHTON WIMBER OF SEQ ID NOS: 19 SOFTWARE: DEACHTON VESION 3.2 SEQ ID NO 18 LENGTH: 79
                                                                                                                                   US-09-954-571-1

US-09-954-571-1

SUBJICTATION OUG US/09954571

SUBJICTATION OUG US/09954571

SUBJICTANT: Chien, Kenneth R

APPLICANT: Chien, Kenneth R

APPLICANT: Hoshijma, Mashiko

APPLICANT: Reds, John

APPLICANT: New Renneth R

APPLICANT: New Renneth R

FILE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER

FILE REREREME 627-PA0123

CURRENT APPLICATION NUMBER: US/09/954,571

CURRENT FILING DATE: 2001-09-11

PRICR PLING DATE: 2000-11-09

NUMBER: OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1

LENGTH: 52:
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Sequence 18, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
APPLICANT: Minamisawa, Susanne
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Meyer, Markus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scott, Christopher
Wang, Yibin
Silverman, Gregg J.
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ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-705-791-18
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                                                                                                       APPLICANT: DILIMIN, WILSGAID
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Sliverman, Gregg J.
ITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
ITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT FILING DATE: 2003-11-02
FRICK APPLICATION NUMBER: 05/106, 718
FRICK FILING DATE: 1998-11-02
FRICK FILING DATE: 1999-11-02
FRICK FILING DATE: 1999-11-02
FRICK FILING DATE: 1999-11-02
FRICK FILING DATE: PASP-11-02
FRICK FILING DATE: PASP-11-03
FRICK FILING DATE: PASP-11-03
FRICK FILING DATE: PASP-11-03
FRICK FILING DATE: PASP-11-03
FRICK FILING 
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APPLICANT: Hoshijma, Masahiko
APPLICANT: Hoshijma, Masahiko
APPLICANT: Mayer, Markus
APPLICANT: Scott, Markus
APPLICANT: Scott, Markus
APPLICANT: Scott, Markus
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF THE SCOTT OF THE TREATMENT
TITLE OF INVENTION NUMBER: 06/106,718
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
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94.7%; Score 71; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%; Score 71; DB 16; Length 35; 100.0%; Pred. No. 6.9e-06; Live 0; Mismatches 0; Indels
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APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
The Regents of the University of California Chien, Kenneth Dillmann, Wolfgang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/10705791
Publication No. US20040121942A1
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Best Local Similarity 100.0'
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US-10-705-791-13
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -10-705-791-12
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LENGIH: 36
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APPLICANT: He, Huaping Mesahiko
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: Hoshijama, Masahiko
APPLICANT: Goott, Christopher
APPLICANT: Mary, Yibin
APPLICANT: Mary, Yibin
APPLICANT: Mary, Yibin
APPLICANT: Scott, Christopher
APPLICANT: Mary, Yibin
APPLICANT: Mary, Yibin
APPLICANT: Mary, Yibin
APPLICANT: Mary, Mary, Mary, Mary, Mary
FILE REFERENCE: 6627-PA9025
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT PILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION UNMBER: PCT/US99/25692
NUMBER OF SEQ ID NOG: 19
NUMBER OF SEQ ID NOG: 19
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Publication Wo. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Coo Yougwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICANT: 003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                          Length 52
                                                                                                                                                                                                                                                                   Query Match
92.0%; Score 69; DB 16; Length 52
Best Local Similarity 93.8%; Pred. No. 2.5e-05;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 6, Application US/10705791
Publication No. US20040121942A1
Publication No. US20040121942A1
APPLICANT: The Regents of the University of California APPLICANT: Chian, Kenneth APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Version 3.2
SEQ ID NO 3
LENGTH: 52
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                                                                                                                                                                      , ORGANISM: Homo sapiens
US-10-705-791-3
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US-10-705-791-6
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LENGTH: 52
                                                                                                                                     TYPE: PRT
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US-10-705-791-4

Sequence 4, Application US/10705791

Sequence 4, Application US/10705791

Sequence 4, Application US/10705791

Sequence 4, Application US/10705791

Sequence 4, Application No. US2040121942A1

SEGUENCE CHIEF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chien, Kenneth
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamiaswa, Susanne
APPLICANT: Minamiaswa, Susanne
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Mayor, Yibin
APPLICANT: Soct, Chriscopher
APPLICANT: Stilverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: 60/106,718
FRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
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                                     0; Gaps
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                             0; Indels
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100.0%; Pred. No. 1.7e-05; attive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEKVOYLTRSAIRRAS 16
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                                                                                                    1 MEKVQYLTRSAIRRA 15
                                                                                                                                                                  1 MEKVOYLTRSAIRRA 15
Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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LENGTH: 52
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Sequence 46161, Application US/10425114

Sequence 46161, Application US/10425114

Sequence 46161, Application US/10425114

Sequence 46161, Application No. US/2004003488A1

GENERAL INFORMATION:
APPLICANT: Lab. Jingdong

APPLICANT: Scoren, Steven E

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Nucleic Acid Molecules (S/10/425,114)

TITLE OF SEQ ID NOS: 73128

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 68
                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.2%; Pred. No. 3.5;
Matches 6; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.7%; Score 41; DB 12; Length 68; Best Local Similarity 71.4%; Pred. No. 5.6; Matches 10; Conservative 0; Mismatches 4; Indels
                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_57573C.1.pep
US-10-424-599-238702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: 701164165_FLI.pep
US-10-425-114-46161
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Sequence 10177, Application US/10156761

Sequence 10177, Application US/10156761

Bublication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIRAMA, UUN
APPLICANT: ISHIRAMA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: APATORI, MASAHIRA
ITILE OF INVANTION: NOVEL POLINUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

WUMBER: OF SEQ ID NOS: 15109
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25 LEKIEYITRERIK 37
                                                                                                                                                                                                                                                                                                                                 1 MEKVOYLTRSAIR 13
                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
SEQ ID NO 238702
                                                                                                            FEATURE:
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; LENGTH: 116
; TYBE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10177
Query Match
Best Local Similarity 46.7%; Pred. No. 10;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEXVQYLTRSAIRRA 15
| | | | | | |
| Db 81 VEXIELVTRGDVRRA 95
Search completed: October 1, 2004, 12:48:42
Job time : 64.4 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

protein search, using sw model OM protein

Run on:

October 1, 2004, 12:05:26 ; Search time 15.6 Seconds (without alignments) 98.658 Million cell updates/sec

US-09-830-779-8 75 1 MEKVQYLTRSAIRRAS 16 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Database :

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|                             |                     |        |        |        |        |        |        |                   |                    |                   |                    |                    |              |        |                    |        |        |                    |                    |                    |        |        |        | _      |                   |                   |                    |                    | •                  |
|-----------------------------|---------------------|--------|--------|--------|--------|--------|--------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------|--------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------|--------|--------|--------|-------------------|-------------------|--------------------|--------------------|--------------------|
| Description                 | id - redme Codopodo | r      | •      | 1      | •      | ı      | ,      | ribosomal protein | phospho-sugar muta | ribosomal protein | probable cell divi | hypothetical prote |              | - 12   | hypothetical prote |        |        | conserved hypothet | probable drup-4-de | hypothetical prote |        |        | G      |        | probable exported | gene PP2A protein | hypothetical prote | transcription init | dishevelled homolo |
| SUMMARIES                   | A40424              | 837638 | A49057 | B40424 | A29002 | 805540 | A39535 | T34780            | F75083             | B70187            | E71104             | B75167             | D69155       | H69179 | F70879             | AC1867 | TOS113 | D69048             | T00104             | A24785             | F83493 | T12833 | H83370 | T04263 | AH1053            | IS5449            | A90253             | JC5425             | 151691             |
| 0.13                        | -                   |        | Н      | -      | Н      | Н      | -      | N                 | 63                 | (1                | 0                  | 0                  | 2            | N      | N                  | ~      | 17     | 0                  | 7                  | 17                 | 63     | 62     | 2      | 7      | 0                 | 7                 | (7)                | 7                  | 0                  |
| .%<br>Query<br>Match Length | 52                  | 52     | 52     | 52     | 52     | 52     | 25     | 116               | 451                | 121               | 1108               | 481                |              |        |                    | 308    | 2712   | 236                | 294                | 335                | 409    | 410    | 417    | 434    | 462               | 486               | 549                | 622                | 736                |
| %<br>Query<br>Match         | 100.0               | 100.0  | 100.0  | 100.0  | 0.96   | 96.0   | 94.7   | 4                 | 54.7               | 53.3              | 53.3               | 52.0               | $\mathbf{c}$ | 49.3   | 49.3               | 49.3   | 49.3   | 48.0               | 48.0               | 48.0               | 48.0   | 48.0   | 48.0   | 48.0   | 48.0              | 48.0              | 48.0               | 48.0               | 48                 |
| Score                       | 75                  | 75     | 75     | 75     | 72     | 72     | 71     | 41                | 41                 | 40                | 40                 | 39                 | 38           |        | 37                 |        | 37     | 36                 | 36                 | 36                 |        |        | 36     |        |                   |                   | 36                 |                    |                    |
| Result<br>No.               | -                   | 7      | e      | 4      | Ŋ      | 9      | 7      | æ                 | თ                  | 10                | 11                 | 12                 | 13           | 14     | 15                 | 16     | 17     | 18                 | 19                 | 20                 | 21     | 22     | 23     | 24     | 25                | 56                | 27                 | 28                 | 59                 |

| hexokinase (EC 2.7 transcription-repahypothetical prote aliphatic amidase transcription regulary proteins and asservation in the cysteine synthase porphobilinogen synthase porphobilinogen synthase porphobilinogen synthase tubblin beta-4 challypothetical proteins bNA-directed RNA phypothetical proteins and proteins a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          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Best Local Similarity
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A; Residues: 1-52 <FUJ>
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A; Accession: I51840
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A, Accession: 337638

A, Molecule type: mRNA

A, Residues: 1-52 < HMAL.

A) Cross-references: EMBL:X71068; NID:9313809; PIDN:CAA50394.1; PID:9313810

R;Johns, D.C.; Feldman, A.M.

B;Johns, D.C.; Feldman, A.M.

B;Johns, D.C.; Feldman, A.M.

B;Johns, D.C.; Feldman, A.M.

B;Johns, D.C.; Feldman, A.M.

A;Title: Identification of a highly conserved region at the 5' flank of the phospholamba

A;Reference number: 152270; MUID:93075183; PMID:1445334

A;Reference number: 152270; MUID:93075183; PMID:1445334

A;Residues: 1-52 < GOHS-

A;Residues: 1-52 < GOHS-

A;Residues: 1-52 < GOHS-

A;Reference number: 151840; MUID:92206563; PMID:1725088

A;Reference number: 151840; MUID:92206563; PMID:1725088

A;Reterence number: 151840; MUID:92206563; PMID:DBJ

A;Reterence number: 151840; MUID:92206563; PMID:AA41845.1; PID:GOMS-

A;Residues: 1-52 HWAA1>
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Fil/Modified site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predict
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
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R;Fulii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
R;Fulii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
A;Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assi
A;Reference number: A40424; MUID:91268032; PMID:1828805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-52 «FUD.
A;Cross-references: GB:W63603; NID:g189942; PIDN:AAA60083.1; PID:g189943
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
C;Comment: Phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation ic;Comment: Helical transmembrane domains of five chains are thought to aggregate in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cipecies: Rattus norvegicus (Norway rat)
Cipacie 105-Mar-1994 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
Cipace 105-Mar-1994 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
Cipacession: S37638; IS2270; IS480; IS580; IS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                 . Species: Homo sapiens (man)
.Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
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100.0%; Pred. No. 5.4e-07;
Live 0; Mismatches 0; Indels
      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:128300; OMIM:172405
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C; Superfamily: phospholamban
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                           phospholamban - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: PLN; PLB
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phospholamban - rabbit (domestic rabbit)

(species: Oryctolagus cuniculus (domestic rabbit)

c)Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999

C)Accession: B40424; S00249

R;Fujii, J; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.

B;Fujii, J.; Zarain-Herzberg, A.; Willard, Br.F.; Tada, C.; MacLennan, D.H.

A;Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assit

A;Reference number: A40424; MUID:91268032; PMID:1828805
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A, Residues: 1-52 «GAN»
A, Residues: 1-52 «GAN»
A, Residues: 1-52 «GAN»
A, Frosser-references: Gardiac muscle
A, Experimental source: Gardiac muscle
A, Note: sequence extracted from NCBI backbone (NCBIN:116999, NCBIP:117001)
C, Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and c; comment: Phosphorylamban is the major phosphorylated protein in cardiac muscle sarcoplasm e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation in C; Superfamily: phospholamban
C, Superfamily: phospholamban
C, Superfamily: phospholamban
C, Superfamily: muscle, muscle; phosphoprotein; tre
A)Accession: 132001.

A)Accession: 132001.

A)Accession: 13201.

A)Accession: 152 AHMA2.

A)Accessions: 1-52 AHMA2.

A)Accessions: 1-52 AHMA2.

A)Accessions: 1-52 AHMA2.

A)Accessions: 1-52 AHMA2.

A)Accessions: 152 AHMA2.

A)
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Accession: A49057
R;Ganim, J.R.; Luo, W.; Ponniah, S.; Grupp, I.; Kim, H.W.; Ferguson, D.G.; Kadambi, V.; N. Circ. Res, 71, 1021-1030, 1992
A;Title: Mouse phospholamban gene expression during development in vivo and in vitro.
A;Reference number: A49057; MUID:93008802; PMID:1394867
A;Accession: A49057
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F)7.1Modified site: acetylated amino end (Met) #status predicted
F)16/Binding site: phosphate (Ser) (covalent) (by cahm-dependent kinase) #status predicte
F)17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status pr
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Matches 16; Conservative
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Gaps

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phospholamban - chicken
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cipate: (O-Mar-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
Ciaccession: A39535; B39535; A44531
R:Toyofuku, T.; Zak, R.
B:Tol. Chem. 266, 5375-5383, 1991
A;Title: Characterization of cDNA and genomic sequences encoding a chicken phospholamban.
A;Reference number: A39535; MUID:91170195; PMID:1825996
                                                                                                                                                                 Ajcross-references: GB:M35393; NID:g164045; PIDN:AAC41618.1; PID:g164046
Cj.Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an Cj.Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an Cj.Comment: Phospholamban is the major phosphorylated and the rate of muscle relaxation; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation; S.Superfamily: phospholamban
Cj.Keywords: acetylated anino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr F;31-52/Domain: transmembrane #status predicted <TMM>
F;1/Modified site: acetylated anino end (Met) #status experiments
F;1/Modified site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status experim F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status e
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A, Residues: 1-52 -VERS.

A; Residues: 1-52 -VERS.

A; Cross-references: EMBL.X15075; NID:92055; PIDN:CAA33171.1; PID:92056

C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and

C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas

C; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation in

C; Superfamily: phospholamban
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F;1/Hodified site: acetylated amino end (Met) #status predicted
F;1/Hodified site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F:10/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Spēcies: Sus sčrofa domestica (domestic pig)
C;bace: 21-Nov-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Accession: SO5540
R;Verboomen, H.; Muytack, F.; Eggermont, J.A.; de Jaegere, S.; Missiaen, L.; Raeymaeke Biochem. J. 262, 33-356, 1989
A;Title: cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle. A;Reference number: SO5540; MUID:90056437; PMID:2530978
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A;Croser-references: GB:NS9039; NID:g212575; FIDN:AAA62738.1; FID:g212576
A;Note: the authors translated the codon CTT for residue 18 as Ile
A;Accession: B39535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.0%; Score 72; DB 1; Length 52; Best Local Similarity 93.8%; Pred. No. 2e-06; Matches 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72; DB 1; Length 52;
Pred. No. 2e-06;
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                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-52 <UY2>
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93.8%;
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Best Local Similarity
Matches 15; Conserv
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    A; Accession: 146227
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                                                                                                                                                                                                                     A. Molecule type: mRNA
A. Residues: 1-52 « PUZ»
A. Cross-references: GB: Y00761; NID:g1661, PIDN:CAA68730.1; PID:g1662
C. Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an C. Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplase; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation it; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phospholamban - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 23-Aug-1987 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Accession: A29002; A26805; A25307; A24818; 146227
C;Accession: A29002; Az6805; Az5307; Az4818; 146227
Figiti, J; Ueno, A; Kitano, K; Tanaka, S.; Kadoma, M.; Tada, M.
J. Clin. Invest. 79, 301-304, 1987
A;Title: Complete complementary DNA-derived amino acid sequence of canine cardiac phosph
A;Reference number: A29002; MUID:87083954; PMID:3793929
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R.Simmerman, H.K.B.; Collins, J.H.; Theibert, J.L.; Wegener, A.D.; Jones, L.R.
J. Biol. Chem. 261, 1333-13341, 1986
A.Title: Sequence analysis of phospholamban. Identification of phosphorylation sites and A.Reference number: A25307, WUID:87008549, PMID:3759968
A.Contents: partial sequence and phosphorylation sites
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R;Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
Nucleic Acids Res. 15, 6738, 1987
A;Title: The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular A;Reference number: A26805; MUID:87316936; PMID:3628007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ajoute: only one gene was detected
Ajoute: the single intron is upstream of the coding region
Ajoute: the single intron is upstream of the coding region
Cjruperfamily: phospholamban
Cjruperfamily: phospholamban
Cjruperfamily: phospholamban
Fig.5.25pomain: transmembrane #status predicted ciruperfamily: phosphore fatus predicted ciruperfamily: phosphore (Ser) (cond (Met) #status predicted
Fig.5.5pomain site: phosphate (Ser) (covalent) (by caMP-dependent kinase) #status
Fig.7/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status
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A;Residues: 10-45 cZIM>
Bicchiu, J.; Kadoma, M.; Toda, H.; Sakiyama, F.
Bicchiem. Biophys. Ree. Commun. 138, 1044-1050, 1986
A;Title: Characterization of structural unit of phospholamban by amino acid sequencing A;Reference number: A24818; MUID:86323152; PMID:3753485
A;Contents: partial sequence and acetylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1.35,'X',37-40,'X',42-45 <FU2>
A;Residues: 1.35,'X',37-40,'X', Radoma, M.; Tada, M.; Tanaka, S.
R;Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
Nucleic Acids Symp. Ser. 17, 121-124, 1986
A;Title: Characterization of recombinant cDNA clones for canine cardiac phospholamban.
A;Reference number: 146227; MUID:87174860; PMID:3562256
                                                                                         the same phospholamban gene.
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Pred. No. 5.4e-07;
; Mismatches 0; Indels
                                          FEBS Lett. 227, 51-55, 1988
A;Title: Rabbit cardiac and slow-twitch muscle express t
A;Reference number: S00249; MUID:88112222; PMID:2962883
A;Accession: S00249
R;Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H.
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Matches 16, Conserv
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A; Residues: 1-52 <FUJ>
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A; Residues: 1-52 < UYE>
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A;Residues: 1-451 «KAM»
X,Cross-references: GB:AL048286; GB:AL096836; NID:gS458366; PIDN:CAB49971.1; PID:gS45848:
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                              435 MEKAEKLVKDAIKKAS 450
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                                                                                                                                                                  C; Superfamily: phosphomannomutase
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Best Local Similarity 53.33
Matches 8; Conservative
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nes 8; Conserva
A;Molecule type: DNA
                                                                                                                                         A; Gene: PAB1666
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E71104
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Cikeywords: deetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F;1/Nodified site: acetylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predict
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
                                                                        A;Note: the sequence of residues 33-52 and the corresponding nucleotide sequence are not R;Toyofuku, T; Zak, R, Sebmitted to GenBank, April 1991
8;Momitted to GenBank, April 1991
A;Reference number: A44531
                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M59038
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
e, after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
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A, Accession: 775083
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A;Experimental source: strain A3(2)
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C,Species: Streptomyces coelicolor
C,Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F75083
R;anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
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R; Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1998
A; Reference number: 221557
A; Accession: T34780
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%; Score 71; DB 1; Length 52; 87.5%; Pred. No. 3e-06; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: the single intron is upstream of the coding region C;Superfamily: phospholamban C;Keywords: acetylated amino end; ATPase inhibitor; muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: rplS; SCOEDB:SC2E1.12
C,Superfamily: Escherichia coli ribosomal protein L19
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: only one gene was detected
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14; Conservative
                            A;Residues: 1-52 <TO2>
A;Cross-references: GB:M59038
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                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-52 < TO3>
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   A; Molecule type: DNA
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Best Local
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C,Genetics:
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T34780
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CiSpecies: Borrella burgdorferi (Lyme disease spirochete)
CiSpecies: Borrella burgdorferi (Lyme disease spirochete)
CiDate: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
CiAccession: B70187
Riverser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Harson, M.; Vugt, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Harch, B. Aauthors: Smith, H.O.; Venter, J.C.
A; Authors: Smith, H.O.; Venter, J.C.
A; Authors: Smith, H.O.; Venter, J.C.
A; Reference number: A70100; MJD:98065943; PMD:9403685
A; Accession: B70187
A; Residues: 1-121 < KLB;
A; Residues: 1-121 < KLB;
A; Residues: 1-121 < KLB;
A; Cross-references: GB:AE00170; GB:AE000783; NID:92688623; PIDN:AAC67044.1; PID:92688625; A; Experimental source: strain B31
C; Superfamily: Bscherichia coli ribosomal protein L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable cell division control protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: E71104
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekint
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic as
A;Reference number: A71000; MUID:98344137; PMID:9679154
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DMA
A;Recidues: 1-1108 «XAM»
A;Recidues: 1-1108 «XAM»
A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29695.1; PID:d1030638; PID:g325701
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A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
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        Length 451;
                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             ribosomal protein L19 (rplS) - Lyme disease spirochete
54.7%; Score 41; DB 2; 50.0%; Pred. No. 12; ive 4; Mismatches
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Cypecies: Mycobacterium tuberuniosis
Cypate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
Cybate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
Cybate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
R;Cole, S.T.; Brosch, R.; Parkhill, V.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
R; Jandrean, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Ammlin, N.; Holroyd, S.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
NATILIE: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: P70879
A;Accession: P70879
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-299
A;Esperimental source: strain H37Rv
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6.Speciaes Nostoc sp. PCC 7120

7.Speciaes Nostoc sp. strain PCC 7120

7.Date: Nostoc sp. strain PCC 7120

7.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

7.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

7.Accession: ACLB67

7.Acamado, N.; Nakamura, Y.; Nolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

7.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A.Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE000842; GB:AE000666; NID:g2621676; PIDN:AAB85107.1; PID:g262168
A;Experimental source: strain Delta H
C;Genetics:
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Referen cumber: A69000; MUID:98037514; PMID:9371463
A;Accession: H69179
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Molecule type: DNA
A;Residues: 1.308 «KUR»
A;Cress-references: GB:BA000019; PIDN:BAB72442.1; PID:g17129829; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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C;Superfamlly: hypothetical protein AF1307
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Best Local Similarity 70.0%
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Cipacies: Pyrococcus abyssi
Cipacies: Pyrococcus abyssi
Cipacies: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
Cipacies: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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A;Molecule type: DNA
A;Residues: 1-119 <MTH>
A;Cross-terences: GB:AE000827; GB:AE000666; NID:g2621489; PIDN:AAB84931.1; PID:g262149
A;Experimental source: strain Delta H
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A;Start codon: TTG
C;Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH425
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50.0%; Pred. No. 30;
tive 3; Mismatches
                                                   668 MEVKDYLTREEVRKA 682
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Best Local Similarity 50.00
Best Local 7; Conservative
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Best Local Similarity
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C,Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 VOYLAEAAIRHNS 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 VELISÝLTOSAI 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 8, Conserva
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Matches 7; Conserv
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Best Local Similarity
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A; Residues: 1-335 < CAP>
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A;Gene: PA1212
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R.Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A.Reference number: A69000; MUID:98037814; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein MTH1364 - Methanobacterium thermoautotrophicum (strain De
C,Species: Methanobacterium thermoautotrophicum
C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-236 <MTH>
A;Cross-references: GB:AE000899; GB:AE000666; NID:g2622468; PIDN:AAB85841.1; PID:g262247
A;Experimental source: strain Delta H
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N;Alternate names: dTDP-4-keto-L-rhamnose reductase
C;Species: Actinobacillus actinomycetemcomitans
                                                                                                                                                                                                                                                                                                              C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05113
R;Brvan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, November 1998
A;Reference number: Z15398
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                                                                              Gaps
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                          49.3%; Score 37; DB 2; Length 308; 53.3%; Pred. No. 44; ive 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: cultivar Columbia; BAC clone F28M20
                                                                                                                                                                                                                                                                                              hypothetical protein F28M20.240 - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Molecule type: DNA
A, Residues: 1-2712 <BEV>
A, Cross-references: EMBL: ALO31004
                                                                                                                                                                          212 LEEVONLVRSVMTRA 226
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                                                                                                                           1 MEKVOYLTRSAIRRA 15
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Best Local Similarity
7, Conserva
                                                    Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 7; Conserv
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A;Introns: 17/3; 24
A;Note: F28M20.240
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                          Query Match
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T00104
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Cylaccession: T00104
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C)Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83493
R;Stover, CK:; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brisadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 955-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathos, A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83493
A;Accession: preliminary
A;Molecule type: DNA
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C;Species: Dictyostelium discoideum
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 18-Jun-1993
C;Accession: A24785
R;Cappello, J; Handelsman, K; Lodish, H.F.
Cell 43, 105-115, 1985
A;Title: Sequence of Dictyostelium DIRS-1: an apparent retrotransposon with inverted term A;Reference number: A94654; MUID:86079481; PMID:2416457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Description: probably catalyzes the reaction of dTDP-6-deoxy-L-mannose + NADP(+) to dTL A,Pathway: dTDP-rhamnose blosynthesis C,Superfamily: dTDP-dihydrostreptose synthase C,Keywords: oxidoreductase
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A, Cross-references: GB: AE004551; GB: AE004091; NID: 99947135; PIDN: AAG04601.1; GSPDB: GN001:
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61.5%; Pred. No. 65;
tive 1; Mismatches
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Pred, No. 91;
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Score 36;
Pred. No.
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      A; Experimental source: strain PAO1
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                                                                                                                          48.0%;
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Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                            154 EQVRWLDREELRRA 167
                                                                                                                                                                                                                                                2 EKVOYLTRSAIRRA 15
                                                                                            Query Match
Best Local Similarity 50...
A: Conservative
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A;Introns: 183/3; 280/3; 316/1
A;Note: F20B18.190
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A; Residues: 1-462 < PAR>
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A; Status: preliminary
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A; Status: preliminary
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A; Molecule type: DNA
                                                              A, Gene: hcnC; PA2195
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A, Residues: 1-104,'V
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A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Roeacule type: DNA
A;Residues: 14410 cLA2
A;Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025547; PIDN:AAC13042.1
R;Kustus; P; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berter
C; Broin; S; Broinilet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V; Carter, N.M.; Cho
A; Ehrlich, B.; Emmerson, P.; Fritz, C.; Fujita, M.; Fujita, Y; Funa, S.; Galizzi, A; Galler
A; Authors: Foulger, D.; Fritz, C; Fujita, M.; Fujita, Y; Funa, S.; Galizzi, A; Galler
Ecch, J; Harwood, C.R.; Henaut, A; Hilbert, H; Holsappel, S; Hosono, S; Hullo, M.F.
Koetter, P; Koningstein, G; Krogh, S; Kumano, M.; Kurita, K; Lapidus, A; Laridnois, A; Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Rivolle, A; Basida, S; Mausel
A; Authors: Lauber, J; Lazarevic, V; Sech, S.; Roche, B.; Roce, M.; Sadaie, Y; Sato, T; Saton, A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Sckiguchi, J; Sekowska, A; Seror akeuchi, M; Tamakoshi, A; Tanaka, T; Terpstra, P; Tognoni, A; Tosato, V; Voshida, R; A; Atthors: Yoshikawa, H; Zumatein, B; Yoshikawa, H; Panchin, A; Danchin, A; Mittel: The complete genome Sequence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                    C;Species: Bacillus subtilis phage SPBC2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C;Accession: T12833; E69915
C;Accession: T12833
C;Accession: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 propha
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83370
C;Accession: H83370
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J., Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. A;Reference number: A82950, MUID: 20437337; PMID: 10984043
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A;Molecule type: DNA
A;Residues: 1-417 <STO>
A;Cross-references: GB:AE004646; GB:AE004091; NID:g9948213; PIDN:AAG05583.1; GSPDB:GN001
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A;Cross-references: GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14016.1; PID:e1183545;
A;Experimental source: strain 168
C;Genetics:
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      Indels
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A, Accession: E69915
      1,
      Mismatches
      1;
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7; Conservative
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                                                           4 VQYLTRSAI 12
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Matches 7; Conserv
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phosphoprotein phosphatase (EC 3.1.3.16) ABII - Arabidopsis thaliana
Nylternate names: protein F20B18.190
C;Speas: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C;Accession: T04263; A54588
C;Accession: T04263; A54588
A;Revan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X
A;Reternce number: 215263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis tha A,Reference number: A54588; MUID:94255767; PMID:8197457
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                                                                                       Gaps
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A;Cross-references: EMBL:AL049483
A;Cross-references: cultivar Columbia; BAC clone F20B18
A;Msyer, K.; Leube, M.P.; Grill, E.
Science 264, 1452-1455, 1994
        DB 2;
Score 36; DB 2
Pred. No. 93;
4; Mismatches
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A; Gene: STY4756
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0 0; Gaps Query Match

48.0%; Score 36; DB 2; Length 462;
Best Local Similarity 53.8%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels

2 EKVQYLTRSAIRR 14 :|| ::|| ||| 294 DKVTWMTREASRR 306

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Search completed: October 1, 2004, 12:19:41 Job time: 20.6 secs

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RESULT 1
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P07473 sus scrofa
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thermoplasm
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blepharisma
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                                                                                                                          October 1, 2004, 12:04:01; Search time 8.8 Seconds (without alignments) 94.673 Million cell updates/sec
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P0099132
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 100 summaries
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Gapop 10.0 , Gapext 0.5
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75
1 MEKVQYLTRSAIRRAS 16
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Match Length
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| Q92356 schizosacch P2366 gallus gall P43207 uria aalge P43208 uria lomvia P43193 alca torda P46801 oryza sativ P46801 oryza sativ P46801 oryza sativ P46801 oryza sativ P46802 vibrio chol P49302 kluvyachonas P63502 vibrio chol P49303 cuscuta ref P69506 calamyacomonas P60506 calamyacom | 899715<br>997215<br>997315<br>9978413<br>99739<br>99739<br>99727<br>99727<br>99727<br>99727<br>9727                                                                                                                                                                                          |
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ALIGNMENTS

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SEQUENCE FROM N.A.
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WEDLINE=2238B257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Atlanent R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Hong L.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Distchenoko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Soares M.B., Donaldo M.F., Casavant T.L., Schetz T.E.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Sedergren E.J., Lu K., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butceffield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Butceffield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Human and mouse cDNA sequences";

"Figure A.C., Grames C.J. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=91268032; PubMed=1828805;
Fujii J., Zarain-Herzberg A., Willard H.F., Tada M., Maclennan D.H.;
"Structure of the rabbit phospholamban gene, cloning of the human
cDNA, and assignment of the gene to human chromosome 6.";
J. Biol. Chem. 266:11669-11675(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITARE-95298769; PubMed=7779806;
Mortishire-Smith R.J., Pitzenberger S.M., Burke C.J., Middaugh C.R., Gareky V.M., Johnson R.G.;
Gareky V.M., Johnson R.G.;
Solution structure of the cytoplasmic domain of phospholamban:
phosphorylation leads to a local perturbation in secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=5526958, PubMed=7749920;
Adams P.D., Arkin I.T., Engelman D.M., Bruenger A.T.;
"Computational searching and mutagenesis suggest a structure for the pencameric transmembrane domain of phospholamban.";
                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                          McTiernan C.F., Frye C.S., Lemster B.H., Kinder B.A., Ogletree-Hughes M.L., Moravec C.S., Feldman A.M.; "The human phospholamban gene: structure and expression."; J. Mol. Cell. Cardiol. 31:679-692(1999).
                                                                                                                                                                                                                                                                                                                 Salvatore C.A., Jacobson M.A.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB).
           52 AA.
             PRT;
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             STANDARD;
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                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                            NCBI_TaxID=9606;
           PPLA_HUMAN
PPLA_HUMAN
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PHOSPHORYLATION (BY PEAL) (BY SIMILARITY).
SIMILARITY).
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Herzyk P., Hubbard R.E.; Using a model of the Using experimental information to produce a model of the length transmembrane domain of the ion channel phospholamban."; Biophys. J. 74:1203-1214(1998).
-!- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.-!- SUBUNIT: Homopentamer.
                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: Membrane.
-:- TISSUB SPECIFICITY: Heart.
-:- PTM: Phosphorylated in response to beta-adrenergic stimulation.
-:- SIMILARITY: Belongs to the phospholamban family.
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Sukaryota, Metacoa; Chordera; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090, 10116, 9986;
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MIM; 172405; ...
InterPro, IPR005984; P lamban.
Pfam; PF04272; Phospholamban; 1.
IIGRFAMs; TIGR01294; P_lamban; 1.
ITGRFAMs; TIGR01294; P_lamban; 1.
Transmembrane; Phospharylation; Abetylation; 3D-structure.
Transmembrane; Phospharylation; CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 75; DB 1; Length 52; 100.0%; Pred. No. 1.3e-07;
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52 AA; 6108 MW; 0766304A76A854D3 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB).
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EMBL; M60411; AAA60109.1; -.
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PDB; 1KCH; 28-NOV-01.
PDB; 1PLP; 31-JUL-95.
PDB; 1PEL; 03-JUL-95.
PDB; 1PSL; 03-UN-95.
Genew; HGNC:9080; PLN.
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AC P20006;
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                                                                                                                                                                                                                                                                                                                                 Pujii J., Lytton J., Tada M., Maclennan D.H.;
Rabbit cardiac and slow-twitch muscle express the same phospholamban
                                                              Fujii J., Zarain-Herzberg A., Willard H.F., Tada M., Maclennan D.H., "Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6."; J. Biol. Chem. 266:11669-11675(1991).
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MEDLINE=33008802; PubMed=1394867;
MEDLINE=33008802; PubMed=1394867;
MEDLINE=33008802; PubMed=1394867;
MEDLINE=33008802; PubMed=1394867;
MEDLINE=3008802; PubMed=1394867;
MEDLINE=3008802; PubMed=1394867;
Med
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-1- FUNCTION: Phospholamban has been postulated to regulate the carcivity of the calcium pump of cardiac sarcoplasmic reticulum.

-1- SUBGNIT: Homopentamer.

-1- SUBGLELULAR LOCATION: Membrane.

-1- TISSUE SPECIFICITY: Heart.

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Shanahan C.M., Weissberg P.L., Metcalfe J.C.;
"Isolation of gene markers of differentiated and proliferating
vascular smooth muscle cells.";
Circ. Res. 73:193-204(1993).
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SPECIES=Rat; TISSUE=Aortic smooth muscle;
MEDLINE=92266263; PubMed=1725098;
MEDLINE=92266263; PubMed=1725098;
MEMANG K.S., Nadal-Ginard B.;
"Cloning phospholamban cDNA from rat aortic smooth muscle.";
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EMBL; M63600; -; NOT ANNOTATED_CDS.
EMBL; M63601; AAA1145.1; -...
EMBL; L03382; AAA1445.1; -...
EMBL; S95849; AAA1849.1; -...
EMBL; S71068; CAA50394.1; -...
EMBL; X71068; CAA50394.1; -...
EMBL; X71068; CAA50394.1; -...
PIR; B49057; A49057.
PIR; B40424; B40444.
                                                                                                                                                                                                                                                                   SPECIES=Rabbit;
MEDLINE=88112222; PubMed=2962883;
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                             MEDLINE=91268032; PubMed=1828805;
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PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
PHOSPHORYLATION (BY CAMK) (BY
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MEDLINE=87316936; PubMed=3628007;
Uyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.;
"The cDNA sequence of the major phospholamban mRNA in canine cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823, 9615,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Tada M.;
"Complete complementary DNA-derived amino acid sequence of canine
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Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
HSSP; P26678; IPLP.
MGD; MGI:97622; Pln.
InterPro; IRR005984; Plamban.
PIGAR, PF04272; Phospholamban; 1.
PIGARPAMS, TIGR01294; Plamban; 1.
Transmembrane; Phosphorylation; Acceylation.
31 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              SIMILARITY).
0763601F76A854D3 CRC64;
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Pred. No. 1.3e-07;
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01-APR-1988 (Rel. 07, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB).
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J. Clin. Invest. 79:301-304(1987).
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MEDLINE=87083954; PubMed=3793929;
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P07473;
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Fri Oct

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SEQUENCE FROM N.A.
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Q82JW4;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES=Pig; TISSUE-Smooth muscle;
MEDLINE=90056437; PubMed=25330978;
MEDLINE=90056437; PubMed=25330978;
Merboomen H., Muytack F., Eggermont J.A., de Jaegere S.,
Missiaen L., Raeymaekers L., Casteels R.;
missiaen L., Raeymaekers L., Casteels R.;
"CDNA cloning and sequencing of phospholamban from pig stomach smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae,
MEDLINE=89291905; PubMed=2544595; Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; "Phospholamban phosphorylation in intext ventricles. Phosphorylation of serine 16 and threonine 17 in response to beta-adrenergic stimulation."; J. Biol. Chem. 264:11468-11474(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 262:353-356(1989).
-!- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.
-!- SUBDNAT: Homopentamer.
-!- SUBCELLULAR LOCATION: Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: Heart.
-!- PTM: Phosphorylated in response to beta-adrenergic stimulation.
-!- SIMILARITY: Belongs to the phospholamban family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation, Acetylation, 3D-structure. 31 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.0%; Score 72; DB 1; Length 52; 93.8%; Pred. No. 4.9e-07; cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY PKA).
PHOSPHORYLATION (BY CAMK1).
076361D9ADC424D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Greated)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cardiac phospholamban (PLB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1FJK; 06-SEP-00.
InterPro; 1PR062984; Plamban.
Pfam; PF04272; Phospholamban; 1.
IIGRFAMS; TIGR01294; P_lamban; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M16012; AAA30884.1; -...
EMBL; Y00399; CAA6846.1; -...
EMBL; M35393; AAC416.1; -...
EMBL; X15075; CAA33171.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 16
17 17
52 AA; 6080 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A29002; A29002.
PIR; S05540; S05540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
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P26677;
                                                                                                                                                                                                                                                                                                                                                                                                                         muscle.";
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACETYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
PHOSPHORYLATION (BY CAMK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                              -:- SUBCELLULAR LÒCATION: Membrane.
-:- TISSUS SPECIFICITY: Heart.
-!- PTM: Phosphorylated in response to beta-adrenergic stimulation.
-:- SIMILARITY: Belongs to the phospholamban family.
MEDINE-91170195; PubMed=1825996;
Toyofuku T., Zak R.;
"Characterization of cDNA and genomic sequences encoding a chicken
                                                                                                         phospholamban.";
J. Biol. Chem. 266.5375-5383(1991).
-!- FUNCTICN: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.
-!- SUBUNIT: Homopentamer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21471403; PubMed=11572949;
MEDLINE=21477403; PubMed=11572949;
Shinose M., Takahashi Y., Horrikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hatcroit M., Shiba T., Sakaki Y., Hatcroit M., Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces avermitilis.
Bacteria; Actinobactéridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1015_TaxID=33303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.7%; Score 71; DB 1; Length 52; 87.5%; Pred. No. 7.6e-07; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P26678; 1rur.
InterPro; IRR055984; P lamban.
Pfam; PF04272; Pb0spholamban; 1.
TIGRFAMS; TIGR01294; P lamban; 1.
Transmembrane; Phosphorylation; Acetylation.
31 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 AA; 6091 MW; F95F86C36A0C4D3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
50S riboscmal protein L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 116 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M59039; AAA62738.1; -.
EMBL; M59037; -; NOT ANNOTATED_CDS.
EMBL; M59038; AAA63167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEKVQYITRSALRRAS 16
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HSSP; P26678; 1PLP.
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nes 14; Conserva
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SPECIES=S.lividans; STRAIN=TK21;
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                                                                                     "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:526-531(2003).

-!-FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).

-!-SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                Ikeda H., Ishikawa J., Haramoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES S. coelicolor; STRAIN=A3(2) / M145;
MEDLINES-1996410, PubMed=12000953;
Bencley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Cronin A., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornaby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Sabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902, 1916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.7%; Score 41; DB 1; Length 116; 46.7%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00402; -; 1.

InterPro; IPR001857; Ribosomal_L19.
Pfam, PF01245; Ribosomal_L19; 1.

PRINTS; PR001661; Ribosomal_L19; 1.

PRODOM; PD002979; Ribosomal_L19; 1.

TIGRRAMs; TIGR01024; rpls bact; 1.

PROSITE; PS01015; RIBOSOMAL_L19; 1.

RIBOSOMAL protein; Complete proteome.

SEQUENCE 116 AA; 13186 NW; 47081773B07F6EB6 CRC64;
SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY 2000 (Rel. 39, Created)
30-MAY 2000 (Rel. 39, Last sequence update)
30-MAY 2000 (Rel. 39, Last sequence update)
50S ribosomal protein L19.
RPLS OR SCOSSES OR SC2E1.12.
Streptomyces coelicolor, and
Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 116 AA
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP005031; BAC70351.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEKVQYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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ID RL19_STF
AC 069883;
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Parro V., Mellado R.P.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
STRAIN=ATCC 35210 / B31;
MIDDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salbards S., Hanson M.,
van Vugr R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:586-586(1997).

-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacy1-tRNA binding site (By similarity).

-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.7%; Score 41; DB 1; Length 116; 46.7%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0061; RIBOSOMALL19.
ProDom; PD002979; Ribosomal L19; 1.
TIGRRAMs; TIGR01024; rplS bact; 1.
PROSITE; PS01015; RIBOSOMAL_L19; 1.
Stibosomal procein; Complete proteome.
SEQUENCE 116 AA; 13142 MW; 37D782C6763D0A90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
508 ribosomal protein L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 286111; CABO6800.1; -. PIR; T34780; T34780. HAMAP; MF 00402; -; InterPro; IPR001857; Ribosomal L19. Pfam; PF01245; Ribosomal L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RL19 BORBU STANDARD; E
OS1642;
15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL939124; CAA19387.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEKVQYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 VEKIELVTRGDVRRA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46...
7, Conservative
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RESULT 10
PSD_CHLCV
                                            Matches
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use by non-profit institutions as long as its content is in no way additied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002318; TRNA-synt_2c.
InterPro; IPR002319; TRNA-synt_Ala.
Pfam; PF01411; TRNA-synt_Zc; 1.
PRINTS; PR00980; TRNA-SYNTHALA.
INGREPAS; ITGR00344; alas; 1.
PR03TE; PS0860; AA TRNA_LIGASE II ALA; 1.
Aminoacyl-tRNA synthetase; Proteïn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1 - CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP + dlphosphate + L-alanyl-tRNA(Ala).
-1 - SUBGELLULAR LOCATION: Cytoplasmic.
-1 - SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruepp A., Granl W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--TRNA ligase) (AlaRS).
ALAS OR TA0849.
                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                    53.3%; Score 40; DB 1; Length 121; 53.3%; Pred. No. 1.7; ive 3; Mismatches 4; Indels
                                                                                                                   HAMAP, ME 00402; -; 1.

InterPro; IPR001857; Ribosomal L19.

Pfam, PF01245; Ribosomal L19; 1.

PRINTS; PR00064; Ribosomal L19; 1.

PRODOM; PD002979; Ribosomal L19; 1.

PROSTE; PS01015; RIBOSOWALL L19; 1.

PROSTE; PS01015; RIBOSOWALL L19; 1.

SROSTE; PS01015; RIBOSOWALL L19; 1.

SROSTER L19; 1.

SROUGHOUG 121 AA; 14011 NW; A33F7B1E4DF24070 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            871 AA; 99907 MW; 6A6B55478463666D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 871 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
                                                                         EMBL; AE001170; AAC67044.1; -. PIR; B70187; B70187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL445065; CAC11978.1; -.
                                                                                                                                                                                                                                                                                                                               1 MEKVOYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                            80 IEKVEVLRRGKVRRA 94
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 407:508-513(2000)
                                                                                                                                                                                                                                                                                   Local Similarity
hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEOUENCE 871 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2303;
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Q9HJW4;
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Matches
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MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., id W. Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002)
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                         Gaps
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0821D3;

10-OCT-2003 (Rel. 42, Created)
110-OCT-2003 (Rel. 42, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65) [Contains:
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0
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52.0%; Score 39; DB 1; Length 871; 69.2%; Pred. No. 22; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBL_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38, DB 1, Length 115, Pred. No. 3.8, 5, Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9EBE9A1B89D3122B CRC64;
                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
505 riboseomal protein Li9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRODOG1; RIBOSOMĀLL19.
ProDom; PD0029; Ribosomal L19; 1.
TIGRFAMS; TIGR01024; rplS bact; 1.
PROSITE; PS01015; RIBOSOMĀL_L19; 1.
RIBOSOMĀL DIOTEIN; COMPLETE PROTEOME.
SEQUENCE 115 AA; 13395 MW; 9EBB9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00402; -; 1.
InterPro; IPR001857; Ribosomal_L19.
Pfam; PF01245; Ribosomal_L19; 1.
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE013104; AAM24679.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 LEKIEVIRRGKVRRA 94
                                                                                                                                                                  353 KVGYLARMLIRRA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 40.0°
Matches 6; Conservative
                                                                                                              3 KVQYLTRSAIRRA 15
                                                         Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
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              Local Similarity
tes 9; Conservat
                                                                                                                                                                                                                                                                                                       THETN
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           Query Match
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RPSD_XANAC
Q8PG33;
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       $2 \text{$\frac{1}{2} \text{$\frac{1} \text{$\frac{1} \text{$\frac{1} \text{$\frac{1} \text{$\frac{1} \text{$\frac{1} \text{$\f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
110-OCT-2003 (Rel. 42, Last annocation update)
110-OCT-2003 (Rel. 41, Last annocation)
(Diadenosine tetraphosphatase) (Ap4A hydrolase) (Diadenosine 5',5'''-
Pl.P4-tetraphosphate pyrophosphodyrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN (BY SIMILARITY).
PHOSPHATIDYLSERINE DECARBOXYLASE ALPHA
CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phospholipid biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHATIDYLSERINE DECARBOXYLASE BETA
                                                                                                                                                                                                                                                                                                                               MEDLINE=22569155; PubMed=12682364;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
                                                                                                   Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83557;
Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 31:2134-2147(2003).
-!- CATALYTIC ACTIVITY: Phosphatidyl-L-serine =
phosphatidylethanolamine + CO(2).
-!- COFACTOR: Pyruvoyl group (By similarity).
-!- SIMILARITY: Belongs to the phosphatidylserine decarboxylase family. Subfamily 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.7%; Score 38; DB 1; Length 299; 43.8%; Pred. No. 11; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6F8EB837D97EE4E0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF 00663; -; 1.
InterPro; IPR003817; PS Dearbxylase.
InterPro; IPR005221; PS decarb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02666; PS_Dcarbxylase; 1.
TIGRFAMs; TIGR00163; PS_decarb; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016997; AAP05666.1; ...
TIGR; CCA00927; -.
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                                   decarboxylase beta chain].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                       PSD OR CCA00927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APAH ACTAC
O52655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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   DDB REAL PROPERTY COLOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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SEQUENCE FROM N.A.

CC 13902 / XV 101;

MEDLINE=2020145; PubMed=1202411;

Ad Silva A.C.R., Ferro J.A., Ferinach F.C., Farah C.S., Furlan L.R.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,

A Cigrelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

A Raid J.B., Ferreira A.S., Ferreira R.C., Ferro M.I.T.,

A Raid J.B., Ferreira A.N.S., Greggio C.C., Gruber A.,

Katuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A Marcins E.C., Medando M.A., Madeira A.M. B.N., Martinez-Rossi N.N.,

Marcins E.C., Medanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

A Peraira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Truffi D., Tsai S.M., White P.F.,

Trindade dos Santos M., Truffi D., Tsai S.M., White P.F.,
                                                                                                                                                                         Saarela M., Fives-Taylor P.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Hydrolyzes diadenosine 5',5'''-Pl,P4-tetraphosphate to yield ADP (By similarity)
-!- CATALYTIC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate + H(2)O = 2 ADP.
-!- SIMILARITY: Belongs to the Ap4A hydrolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.3%; Score 37; DB 1; Length 275; 40.0%; Pred. No. 15; tive 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 AA; 31480 MW; 0843F4FE11FF6DAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
RMA polymerase sigma factor rpoD (Sigma-70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; NF_00199; -; 1.
InterPro; IPR004617; ApaH.
InterPro; IPR004843; M-ppestrase.
InterPro; IPR006186; T_phtase_apaH.
Pfam; PF00149; Metallophos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000252; T_phtase_apaH; 1.
TIGRFAMS; TIGR00668; apaH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF043998; AAC00202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 EDKÖYFTQSAVKKSN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EKVQYLTRSAIRRAS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=92829;
                                                            NCBI_TaxID=714;
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Setubal J.C., Kitajima J.P.; "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."; Nature 417:459-463(2002).
                                                                                                                                                                    -1- FUNCTION: The sigma factor is an initiation factor that promotes attachment of the RNA polymerase to specific initiation sites and then is released. This is the primary sigma-factor of this bacteria (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=AS-3;
MEDLINE=9725706; PubMed=9103980;
Salvini M., Bini E., Santucci A., Batistoni R.;
Salvini M., Bini E., Santucci A., Batistoni R.;
Tilophora, Heterotrichida).";
FEMS Microbiol. Lett. 149:93-98(1997)
-!- FUNCTION: Histone H4,
-in nucleosome formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00715; SIGNA70_1; 1.
PROSITE; PS00716; SIGNA70_2; 1.
Transcription regulation; Signa factor; DNA-directed RNA polymerase;
DNA-binding; Complete proteome.
DOMA-IN 414 427 POLYMERASE CORE BINDING (POTENTIAL).
NNA NIND 584 603 H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota, Alveolata; Ciliophora; Heterotrichea; Heterotrichida;
Blepharismidae; Blepharisma.
NCBI_TaxID=5961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6B7032460884C850 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMEL; AEGOLOST, AAMSB630.1; -... EMEL; AEGOLOST, AAMSB630.1; -... InterPro; IPR009043; RNA_polsigma. InterPro; IPR001631; Sigma70_ner. InterPro; IPR00127; Sigma70_r1.

InterPro; IPR009042; Sigma70_r2.

InterPro; IPR007627; Sigma70_r2.

InterPro; IPR007637; Sigma70_r2.

R InterPro; IPR007630; Sigma70_r3.

R InterPro; IPR000943; Sigma70_r4.

R Pfam; PP04546; Sigma70_ner.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Figure 1 F0037, saggma70_r1_2; Pfam; PF004542; sigma70_r2; 1. Pfam; PP04542; sigma70_r2; 1. Pfam; PP04545; sigma70_r4; 1. PRINTS; PR00046; SIGMA70FCT.
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P80738;
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SEQUENCE
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Matches
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         SOTTEM SET THE SOURCE OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salvini M., Bini E., Santucci A., Batistoni R.;
"H4 histone in the macronucleus of Blepharisma japonicum (Protozoa,
Ciliophora, Heterotrichida).";
FEMS Microbiol. Lett. 149:93-98 (1997)
-!- FUNCTION: Histone H4, along with histone H3, plays a central role
in nucleosome formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
-!- SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS, PROD623, HISTONEH4.
Prodom; PD001827, Histone_H4; 1.
SWART; SM00417, H4; 1.
PROSITE; PS00047, H1STONE_H4; PARTIAL.
Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
NON TER
                                                                                                        InterPro; IPR01951; Histone H4.

PRINTS, PR00623; HISTONEH4.

ProDom; PD001827; Histone H4; 1.

ProSITE; PS00047; HISTONE H4; PARTIAL.

Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding. NON TER 47 47 47 87 8200ENCE 47 AA, 4961 MW; D743BEA73B76BADA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blepharisma japonicum.
Eukaryota, Alveolata, Ciliophora, Heterotrichea, Heterotrichida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                        48.0%; Score 36; DB 1; Length 47; 53.8%; Pred. No. 3.5; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 AA; 10722 MW; 64BBB2D65594607C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the histone H4 family.
                                                     bp of DNA.
-!- SIMILARITY: Belongs to the histone H4 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-46, AND SEQUENCE OF 9-97 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H41 BLEJA
P80737; P90515;
01-NOV-1997 (Rel. 35, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007124; Hist TAF.
InterPro; IPR007125; Histone_core_D.
InterPro; IPR001951; Histone_H4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A5-3;
MEDLINE=97257506; PubMed=9103980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blepharismidae, Blepharisma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X97995; CAA66634.1;
                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 53.84
Conservative
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EKVOYLTRSAIRR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 ÉNIÓGITKPÁÍRR 39
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H41 BLEJA
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P2C1_ARATH
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                                                                                                                                                                                                                                                                                                                                              Genome Res. 13:1572-1579(2003).
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacy1-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                          "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
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                                                                                                                                                                       Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L19.
RPLS OR CALASO37.
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.0%; Score 36; DB 1; Length 113; 40.0%; Pred. No. 9.1; ive 5; Mismatches 4; Indels
                                                                                                                                                                                             Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9BD1C9D25ADA453A CRC64;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 1231C / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                                          15-MAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
50S ribosomal protein L19.
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InterPro: IRRO1857; Riboscmal L19.
Fram. PF01245; Riboscmal L19.
PRINTS; PR00661; RIBOSCMALL19.
ProDom; PD002979; Riboscmal L19; 1.
IGMRAMS; TIGR01024; rp1S_bct; 1.
PROSITE; PS01015; RIBOSCMAL L19; 1.
Riboscmal protein; Complete proteome.
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               6; Conservative
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EKVQYLTRSAIRR
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                                                                                                                                                                                  "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
interface and may play a role in the structure and function of the
aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meyer K., Leube M.P., Grill E., "A protein phosphates 2C involved in ABA signal transduction in Arabidopsis thaliana.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia, TISSUB=Leaf;
MEDLINES=95007788; PubMed=7922358;
Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
Mindrinos M., Katagiri F., Yu G.L.
"The A. thaliana disease resistance gene RP82 encodes a protein containing a nucleotide-binding site and leucine-rich repeats.";
[31] 78:1089-1099(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 113;
Pred. No. 9.1;
5; Mismatches 4; Indels
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InterPro; IPR01857; Ribosomal 119.
Pfam, PF01245; Ribosomal 119; 1.
PRINTS; PR00061; Ribosomal 119; 1.
PRINTS; PR00061; Ribosomal 119; 1.
PRODOM; PD002979; Ribosomal 119; 1.
PROSITE; PS01015; RIBOSOMAL 119; 1.
RRIDSSOMAL 119; 1.
SEQUENCE 1113 AA; 12875 MW; 2692B361BAFBA229 CRC64;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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STRAIN=cv. Landsberg erecta;
MEDLINE=94255767; PubMed=8197457;
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80 IEKIEVIRRGDVRRA 94
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Best Local Similarity
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                                                                                                                              'Arabidopsis ABA response gene ABI1: features of a calcium-modulated
                         STRAIN=cv. Columbia; TISSUE=Leaf;
MEDLINE=94255766; PubMed=7910981;
Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F.,
                                                                                                                                                          orotein phosphatase.";
Science 264:1448-1452(1994).
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STRAIN=cv. Columbia;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                          Giraudat J.
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182 24 G -> R (IN REF. 5).

105 105 1 -> V (IN REF. 1).

434 AA; 47505 MW; 4A4C54F04195F572 CRC64;
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4 POLY-VAL.
                                                                                                                                                                  phosphate.
-!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
-!- SIMILARITY: Belongs to the PP2C family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, alpha isoform (PP2A, B subunit, B' alpha isoform) (PP2A, B subunit, PR61 alpha isoform) (PP2A, B subunit, PR61 alpha isoform) (PP2A, B
   Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                               signaling pathway.

    -i- FUNCTION: Involved in abscisic acid (ABA) signaling pathw
    -i- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein

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4; Mismatches
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MEDLINE=96064678; PubMed=7592815;
McCright B., Virshup D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ", U12856; AAA50237.1; -...
", X77116; CAA54383.1; -...
", AL049483; CAB39673.1; -...
", AL161564; CAB79463.1; -...
", AY035073; AAK59578.1; -...
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InterPro; IPR002048; EF-hand.
InterPro; IPR001932; PP2C-like.
InterPro; IPR000222; PP2C.
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SMART; SMO0331; PP2C SIG; 1.
SMART; SM00332; PP2CC; 1.
PRCSTIE; PS00018; EF HAND; 1.
PROSITE; PS01032; PP2C; 1.
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                                                                                       Science 302:842-846(2003).
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HSSP; P35813; 1A60.
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Yuan S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPP2R5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 18
2A5A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
```

624 AA

STANDARD;

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUENCE TROM N.A.

RA

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertollin M.C., Camargo L.B.A.,

RA Alves L.M.C., Cannavan F., Cardozo J., Chambergo F.C., Ciapina L.P.,

RA Enria J.B., Ferraina A.J.S., Ferraina R.C.C., Ferron M.I.T.,

RA Enria J.B., Ferranco M.C., Gareggio C.C., Ferron M.I.T.,

RA Envyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Estyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Estyama A.M., Madeira A.M.B.M., Mayaki C.Y., Moon D.H.,

Noreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D.S., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Taunra R.E., Teixeira B.C.,

Setubal J.C., Kitajima J.P.,

Setubal J.C., Kitajima J.P.,

Noret specificities G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 417:459-463(2002).

-!- FUNCTION: The sigma factor is an initiation factor that promotes attachment of the RNA polymerase to specific initiation sites and then is released. This is the primary sigma-factor of this bacteria (By similarity).

-!- SIMILARITY: Belongs to the sigma-70 factor family.
                                                                                                                                                  Xanthomonas campestris (pv. campestris).
Bacteria; Protecbacteria; Gammaprotecbacteria; Xanthomonadaceae; Xanthomonadaceae; Xanthomonas.
                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RNA Polymerase sigma factor rpoD (Sigma-70).
                                                                                                                                     RPOD OR XCC3736.
                                                                                                                                                                                                        NCBI_TaxID=340;
                                 RPSD XAN
Q8P4HZ;
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM) *01643; -.
GO; GO:0005737 C:cytoplasm; TAS.
GO; GO:0008601; F:protein phosphatase type 2A, intrinsic regu. . .; TAS.
InterPro; IPR008938; ARM.
InterPro; IPR002554; B56.
                                                                                                                                                                                                                                                                                                                                                                                                                     SUBDINIT: PP2A consists of a common heterodimeric core enzyme, COMPOSED of a 36 kDa catalytic subunit (subunit C) and a 65 kDa constant regulatory subunit (PR65 or subunit A), that associates with a variety of regulatory subunits. Proteins that associate with the core dimer include three families of regulatory subunits B (the R2/B/PR55/B55, R3/Br /PR72/PR130/PR59 and R5/B/B56 families), the 48 kDa variable regulatory subunit, viral proteins, SUBCELLULAR LOCATION: Cytoplasmic.

TISSUE SPECIFICITY: Widely expressed with the highest expression in heart and skeletal muscle.
                                                                                                                        Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I., Merlevede W., Goris J., Hemmirgs B.A.;
"The variable subunit associated with protein phosphatase 2A0 defines a novel multimember family of regulatory subunits.";
Biochem. J. 317:187-194(1996).
"Identification of a new family of protein phosphatase 2A regulatory
                                                                                                                                                                                                                                             MEDLINE=96355607; The PubMed=8703017; McCright B., Rivers A.M., Audlin; S., Virshup D.M.; Trivers A.M., Audlin; S., Virshup D.M.; The BS6 family of protein phosphatase 2A (FP2A) regulatory subunits encodes differentiation-induced phosphoproteins that target PP2A to both nucleus and cytoplasm.";
                                                                                                                                                                                                                                                                                                                                 U. Biol. Chem. 271:22081-22089(1996).
-!- FUNCTION: The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: Phosphorylated on serine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> F (IN REF. 2; AA SEQUENCE)
-> S (IN REF. 2; AA SEQUENCE)
-> E (IN REF. 2; AA SEQUENCE)
D31407F7032A6D44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 486;
                                                                    SEQUENCE OF 47-56; 129-132; 347-354; 448-462 AND 471-480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1
Pred. No. 44;
3; Mismatches
                                                                                                                                                                                                                                PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
                      subunits.";
J. Biol. Chem. 270:26123-26128(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation; Multigene family.

DOMAIN

2 5 POLY-SER.
                                                                                       TISSUE=Brain;
MEDLINE=96276417; PubMed=8694763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52
54
H
451
F6193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L42373; AAC37601.1; -. PIR; I55449; I55449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:9309; PPP2R5A.
MIM; 601643; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01603; B56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
54
451
486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                  BMBL; AE012494; AAM42993.1; -..

RINGEPPC; IPR009043; RNA_DOl_sigma.
InterPrc; IPR009043; RNA_DOl_sigma.
InterPrc; IPR009042; Sigma70_ner.
RINGEPPC; IPR009042; Sigma70_r1_2.
RINGEPPC; IPR007624; Sigma70_r2.
RINGEPPC; IPR007624; Sigma70_r2.
RINGEPPC; IPR007630; Sigma70_r4.
RINGEPPC; IPR00943; Sigma70_r4.
RINGEPPC; IPR00943; Sigma70_r1_1; 1.
R Pfam; PF00140; Sigma70_r1_1; 1.
R Pfam; PF04542; Sigma70_r2; 1.
R Pfam; PF04542; Sigma70_r2; 1.
R Pfam; PF04545; Sigma70_r2; 1.
R Pfam; PF04545; Sigma70_r2; 1.
R RRINTS; PR0016; SIGMA70_r4; 1.
R PROSITE; PS00716; SIGMA70_2; 1.
W Transcription regulation; Sigma factor; DNA-directed RNA polymerase; M DNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYMERASE CORE BINDING (POTENTIAL)
502 H-T-H MOTIF (BY SIMILARITY).
69947 MW; 1F6C8CA093F7F1AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       624 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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Query Match

; 0

Gaps

. 0

4; Indels

2 EKVOYLTRSAIRRA 15 EKVDGFTRKSVRKA 32

δ ద

19

7; Conservative

Local Similarity

Length 624; DB 1; Score 36; 48.0%;

RESULT 19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DCT-2003 (Rel. 42, Last annocation update)
Magnesium-chelatase subunit chlD (Mg-protoporphyrin IX chelatase) (Mg-
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Involved in chlorophyll biosynthesis, introduces a magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
                                                                                                                                                                                                                                                                                                                                                                                                    Masuda T., Nakayama M., Ohta H., Takayama K.-I., "Cloning and sequencing of a chib gene encoding a subunit of magnesium-chelatase from the cyanobacterium Synechococcus sp. PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Chlorophyll biosynthesis.
-!- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
-!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                              Janechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
11.1 — PaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.0%; Score 36; DB 1; Length 677;
58.3%; Pred. No. 63;
Live 2; Mismatches 3; Indels
                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00382; AAA; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS50234; VWPA; 1.
PROSITE; PS50234; VWPA; 1.
DOMAIN 481 676 VWPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7E2988E096DF5506 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                           PRT; 677 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 736 A.A.
 50.0%; Pred. No. 57; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLU/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB003135; BAA20346.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR00523; Wg_A.
InterPro; IPR002035; VWF_A.
Pfam; PF01078; Mg_chelatase; 1.
Pfam; PF01078; Wa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (In) Plant Gene Register PGR97-091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 676 VI
329 383 GI
677 AA; 73367 MW;
                                                                                    357 MEKANYLTLAEIKDIS 372
                                                    1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 58.3.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 EQIGYLVREAIR 278
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EKVOYLTRSAIR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                 chelatase subunit D)
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                           CHLD SYNP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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DVL2_XENLA
ID DVL2_XENI
AC P51142;
                                                                                                                                       RESULT 20
CHLD_SYNP7
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                                                                                                                                                                                                                                                                                                MEDILINE=96017659; PubMed=7588081;
A Sokol S.Y., Kilngensmith U., Perrimon N., Itoh K.;
Bokol S.Y., Kilngensmith U., Perrimon N., Itoh K.;
Development 121:3487.3487(1995).

-!- FUNCTION: May play a role in the signal transduction pathway mediated by multiple Wnt genes. Plays a role in dorsal axis formation and in neural induction.

-!- FUNCTION: Capplesmit (Potential).

-!- SUBCELULIAR LOCATION: Cytoplasmic (Potential).

-!- TISSUE SPECIFICITY: Ubiquitous protein found equally distributed in both animal vegetal and dorsal-ventral directions.

-!- DEVELOPMENTAL STAGE: Maternal gene detected in different developmental stages being most abundant in eggs.

-!- SIMILARITY: Belongs to the DSH family.

-!- SIMILARITY: Contains 1 DEP domain.

-!- SIMILARITY: Contains 1 DEX domain.
Segment polarity protein dishevelled homolog DVL-2 (Dishevelled-2) (DSH homolog 2) (Xdsh).
                   (DŠH homolog 2) (Kásh).
Kanopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                               Sokol S.Y., Klingensmith J., Perrimon N., Itoh K.; "Dorsalizing and neuralizing properties of Kdsh, a maternally expressed Xenopus homolog of dishevelled."; bevalopment 121:1647(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF6C9A1662DD7CEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.
Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-PRO. POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSF; Q12923; 3PDZ.
InterPro; IPR000599; DEP.
InterPro; IPR000539; Dishevell.
InterPro; IPR003331; Dishevelled.
InterPro; IPR003341; Dishevelled.
InterPro; IPR001158; DIX.
InterPro; IPR001478; DIX.
InterPro; IPR001478; PDZ.
Pfam; PF00510; DRP; 1.
Pfam; PF00578; DIX; 1.
Pfam; PP00778; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-PRO
                                                                                                                                                            TISSUE=Oocyte;
MEDLINE=95324391; PubMed=7600981;
MEDLINE=95324391; PubMed=7600981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01760; DISHEVELLED.
PRINTS; PR01762; DISHEVELLED2.
ProDom; PD003639; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U31552; AAB00688.1; -. PIR; I51691; I51691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0186; DEP; 1.
PROSITE; PSS0841; DIX; 1.
PROSITE; PSS0106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMARI, SM00021, DAX, 1.
SMARI, SM00049, DEP, 1.
SMARI, SM00228, PDZ, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wnt signaling pathway;
                                                                                         Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222
254
428
680
736 AA;
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                           NCBI_TaxID=8355;
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SEQUENCE
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48.0%; Score 36; DB 1; Length 736;

Query Match

924 AA; 100253 MW; 0162C1591AF040AC CRC64;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White J.A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + D.hexose = ADP + D.hexose 6-phosphate.
-!- ENZYME REGULATION: Hexokinase is an allosteric enzyme inhibited by
                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANBOUS: In vertebrates there are four major glucose-phosphorylating isoenzymes, designated hexokinase I, II, III and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: First step of several metabolic pathways.
-!- SUBUNIT: Monomer.
-!- SUBUNIT: Monomer.
-!- BOWAIN: THE N- AND C-TERMINAL HALVES OF THIS HEXOKINASE SHOW EXTENSIVE SEQUENCE SIMILARITY TO EACH OTHER. THE CATALYTIC ACTIVITY IS ASSOCIATED WITH THE C-TERMINUS WHILE REGULATORY FUNCTION IS ASSOCIATED WITH THE N-TERMINUS.
                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schwab D.A., Wilson J.B.; "Complete amino acid sequence of the type III isozyme of rat "Complete amino acid sequence of char charkinase, 'deduced from the cloned cDNA"; Arch. Elochem. Blophys. 285:365-370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P05708; LEG3.
InterPro; IPR001312; Hexokinase.
Pfam; PF03127; hexokinase.; 2.
Pfam; PF0349; hexokinase; 2.
PRINTS; PR00475; HEXOKINASE.
PRODOM; PD001109; HEXOKINASE.
PROSTIE; PS00378; HEXOKINASE; 2.
Transferase; Kinase; Glycolysis; Allosteric enzyme; Repeat; ATP-binding; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC.
GLUCOSE-BINDING (POTENTIAL).
GLUCOSE-BINDING (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the hexokinase family.
                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Hexokinase type III (EC 2.7.1.1) (HK III).
     Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91378267; PubMed=1897938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U73859; AAB18253.1; -.
70.0%;
                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its product Glc-6-P.
                                                                                                                                                                                STANDARD;
                                                                                          624 EYSTRSSIRR 633
                                                         5 QYLTRSAIRR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (glucokinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; S13913; S13913.
     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=10116;
                                                                                                                                                                                HXK3 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
DOMAIN
NP BIND
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                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R InterPro; IPR007121; RNA_pol_B.

R InterPro; IPR007644; RNA_pol_Rpb2_1.

R InterPro; IPR007644; RNA_pol_Rpb2_2.

R InterPro; IPR007642; RNA_pol_Rpb2_2.

R InterPro; IPR007641; RNA_pol_Rpb2_2.

R InterPro; IPR007641; RNA_pol_Rpb2_7.

R Pfam; PF04563; RNA_pol_Rpb2_7.

R Pfam; PF04563; RNA_pol_Rpb2_2; 1.

R Pfam; PF04560; RNA_pol_Rpb2_2; 1.

R Pfam; PF04560; RNA_pol_Rpb2_7; 1.

R PGSTIE; PS011666; RNA_pol_Rpb2_7; 1.

R PGSTIE; PS011666; RNA_pol_Rpb2_7; 1.

R PGSTIE; PS011667; RNA_pol_Rpb2_7; RNA_pol_Rpb2_7; RNA_pol_Rpb2_7; RNA_pol_Rpb2_7; RNA_pol_Rpb2_7; RNA_pol_Rpb2_7; RNA_pol_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {RNA}(N).
-!- SUBJUNT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beta', and beta',
-!- SUBJULIAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20150907; PubMed=10688199;
Lemieux C., Otis C., Turmel M.;
"Ancestral chloroplast genome in Mesostigma viride reveals an early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of DNA into RNA using the four ribonuclecside triphosphates as
                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
Mesostigmatales; Mesostigmataceae; Mesostigma.
NCBI_TaxID=41882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.0%; Score 36; DB 1; Length 1080;
43.8%; Pred. No. 1e+02;
tive 6; Mismatches 3; Indels
Query Match
Best Local Similarity 61.5%; Pred. No. 88;
Matches 8; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-directed RNA polymerase beta chain (BC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                 PRT; 1080 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              branch of green plant evolution.";
Nature 403:649-652(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF166114; AAF43826.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                       638 ODVVÝLLREÁTŘŘ 650
                                                                                                                           2 EKVQYLTRSAIRR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 43.8 es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9KWU7; 1HOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesostigma viride.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 RPOB MESVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                 RESULT 23
RPOB MESVI
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us-09-830-779-8.rsp

0

Gaps

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Drosophila melanogaster (Fruit fly).
Bukaryota, Metezoa, Arthropoda, Hexapoda; Insecta; Pterygota,
Neoptera, Endopterayota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                             09VZS5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
60S ribosomal protein L28.
                                                                                                                                         144 AA
                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
::::| |::|||||
66 LKRPKYNERTSIRRAS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 287:2185-2195(2000).
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Berkeley;
                                                                                                                                         RL28 DROME
                                                                                                                                                                                                                                                                               CG12740.
                                                                                              RESULT 24
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HERE BERNE B

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                                                                                                                                                                                                                                                  EMBL; AYO71444; AAL49066.1; -.
EMBL; AYO71444; AAL49066.1; -.
FlyBame; FBGM003542; CG12740.
GO; GO: 0005942; CGytosolic large ribosomal subunit (sensu Eu. . ; ISS.
GO; GO: 0003735; F: structural constituent of ribosome; ISS.
GO; GO: 0006412; P: protein biosynthesis; ISS.
InterPro; IPR002672; Ribosomal_L28e.
Figm; PF01778; Ribosomal_L28e; 1.
ProDom; PD010767; Ribosomal_L28e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99437995; PubMed=10508151;
O'Hara B.P., Norman R.A., Wan P.T., Roe S.M., Barrett T.E., Drew R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAINS-ATCC 15692 / PAO1;
STRAINS-ATCC 15692 / PAO1;
STRAINS-ATCC 15692 / PAO1;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagron M.,
Garber, R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lorry S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lowe N., Rice P.M., Drew R.E.; "Nucleotide sequence of the aliphatic amidase regulator gene (amiR) of Pseudomonas aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson S.A., Drew R.E.; "Transcriptional analysis of the amidase operon from Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF COMPLEX WITH AMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.7%; Score 35; DB 1; Length 144; 70.0%; Pred. No. 18; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 AA; 16029 MW; 14D5C7866F585113 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1989 (Rel. 11, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Aliphatic amidase regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 177:3052-3057(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89211409; PubMed=2495988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
MEDLINE=95286483; PubMed=7539417;
                                                                                                                                                                                                                              EMBL; AE003477; AAF47742.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett, 246:39-43(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 70.0
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 LTOAALRRAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIR OR PA3363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=PAC433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIR PSEAE
P10932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
       ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A PART THE REAL PARTS AND THE REAL PROPERTY AND THE REAL PARTS AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=ZOLYGOUGE, FUNDED-101112.;

AMEDLINE=ZOLYGOUGE, FUNDED-101112.;

AMEDLINE=ZOLYGOUGE, FUNDED-101112.;

AMEDLINE=ZOLYGOUGE, FUNDED-101112.;

AMEDLINE=ZOLYGOUGE, FUNDED-10112.;

AMEDLINE=ZOLYGOUGE, FUNDED-10112.;

BENDER R.A., Icalia S.E., Richards S., Ashburner M., Henderson S.N., Sutron G.C., Wortman J.R., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y. H.C., Blazej R.G., Champpe M., Pfelifer B.D.,

RA Abril J.F., Apdravan, P. An H.-J., Andrews Pfennkoch C., Baldwin D.,

Ballew R.M., Basu A., An H.-J., Andrews Pfennkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxen B.P., Bhandari D., Bessley E.M.,

Besson K.Y., Bence P.V., Berman B.P., Cadieu E., Center A., Chandra I.,

RA Borkova D., Botchan M.R., Bouck J., Broxetier P.,

Burtis K.C., Busam D.A., Bulke C., Davenport L.B., Davies P.,

R. Borkova D., Botchan M.R., Bouck J., Broxetier P.,

Burtis K.C., Busam D.A., Bulke C., Derraz C., Ferriac S., Botchan N.,

RA Cherry J.M., Cawley S., Dahlke C., Derraz C., Ferriac S., Dunne P.,

Burtis K.C., Boung L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Faragelista C.C., Ferriac S., Paris C., Brischman W.,

RA Durbin K.J., Barnes M., Bouck J., Harris M.,

Harris N.L., Harvey D.A., Hewland T.J., Hei M.-H., Ibegwam C.,

RA Harris N.L., Harvey D.A., Hewland T.J., Hei M.-H., Ibegwam C.,

RA Lasko P., Lei, Y., Levitsky A.A., Li J.H., Li Z., Liang Y.,

Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai S.,

Rand E., Nelson K.A., Howland T.C., Morris J., Morsty D., Northerson D.,

Relicu X., Nelson K.A., Howler B., Worter B., Shell H.,

Rhue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.,

Rang Z.-Y., Wassarman D.A., Wenter E., Wang S., Yao Q.A.,

Wang Z.-Y., Wassarman D.A., Weiter J.C.,

Rober R., Myers B.W., Rubin G.M., Venter J., Sin X., Smith H.O.,

R., Shore R.M., Myers B.W., Rubin G.M., Venter J., Since P., Shill R.J., Weilber S., Shill R.J., Weilber S., Shill R.J., Weilber S., Shill R.J., Shill R.J., Shill R.J., Shill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                 EMBL, X13776; CAA32023.1; -.
EMBL, AE004758; AAG06751.1; -.
PIR, B93226; B83226.
PIR, 503884; S03884
PDB; 1000; 23-DEC-99.
InterPro; IPR005561; ANTAR.
InterPro; IPR003127; Res_reg_antiterm.
PIRSF; PIRSF036327; Res_reg_antiterm.
PIRSF; PIRSF036327; Res_reg_antiterm; 1.
Transcription regulation; Transcription antitermination; 3D-structure;
                                                  -i- FUNCTION: Positive controlling element of amiE, the gene for alightatic amidase. Acts as a transcriptional antitermination factor. It is thought to allow RNA polymerase read through a rhoindependent transcription terminator between the amiE promoter and
          "Crystal structure and induction mechanism of AmiC-AmiR: a ligand-regulated transcription antitermination complex."; EMBO J. 18:5175-5186(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.7%; Score 35; DB 1; Length 196; 53.8%; Pred. No. 26; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21903 MW; 306A4F30E8E4C6C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  REF.
REF.
                                                                                                                                                                                                                                                                                                                                                                                                   HERRE
                                                                                                        gene.
SUBUNIT: Forms a complex with amiC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.83
Matches 7; Conservative
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196 AA;
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| Description                   | Q82jw4 streptomyce | Q9uzt5 pyrococcus | Q9q6q3 grapevine l | Oscfm4 mus musculu | 087993 vibrio para | 058310 pyrococcus | Q9a0y9 streptococc | Q88111 pseudomonas | Q9am36 desulfovibr | Q9v1d2 pyrococcus | Q868u8 euplotes ae | 026525 methanobact | 0974n9 sulfolobus | Q89j03 bradyrhizob | O7ufr1 rhodopire11 | Q9hf62 ashbya goss |  |  |
| SUMMARIES                     | Q82JW4             | Q9UZT5            | Q9Q6Q3             | Q8CFM4             | Q87GQ3             | 058310            | Q9A0Y9             | Q88LL1             | Q9AM36             | Q9V1D2            | Q868U8             | 026525             | Q974N9            | Q89J03             | Q7UFR1             | Q9HF62             |  |  |
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| %<br>Query<br>Match           | 54.7               | 54.7              | 53.3               | 53.3               | 53.3               | 53.3              | 52.0               | 52.0               | 52.0               | 52.0              | 52.0               | 50.7               | 50.7              | 50.7               | 50.7               | 50.7               |  |  |
| Score                         | 41                 | 41                | 40                 | 40                 | 40                 | 40                | 39                 | 39                 | 39                 | 39                | 39                 | 38                 | 38                | 38                 | 38                 | 38                 |  |  |
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RESULT 3
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                                                                                 Q97wf6 homo sapien
Q8cs49 staphylococ
Q9ars3 volvox cart
Q9lvul arabidopsis
Q82c01 streptomyce
Q832p8 enterococu
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0
                                                  Q8yw51 anabaena sp
Q92ry5 rhizobium m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8pn39 xanthomonas
                 Q30735 macaca neme
                                   Q8iy90 homo sapien
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MEDLINE-21477403, PubMed-11572948;

Omuta S., Ireda H., Ishikawa U., Hanamoto A., Takahashi C.,

Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,

Kikuchi H., Shiba T., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces
avermitils: deducing the ability of producing secondary
metabolites.";

Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces avermitilis.
Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
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MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                             PRT; 116 AA
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Putative ribosomal protein L19.
RPLS OR SAV2640.
               Q30735
Q81Y90
Q8YW51
Q92RY5
Q9NWF6
Q8CS49
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082C01
0832P8
Q8 PN3 9
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RESULT 2

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GQ GO: 00106868; F:intramolecular transferase activity, phosph. . .; IEA. GO; GO: 00106868; F:intramolecular transferase activity, phosph. . .; IEA. INCO GO: 005975; P:carbohydrate metabolism; IEA. INTERPRO; IPRO05841; PG PMM ABAI. INTERPRO; IPRO05844; PG PMM ABAII. INTERPRO; IPRO05845; PG PMM ABAII. INTERPRO; IPRO05843; PG PMM, ABAIII. INTERPRO; IPRO05843; PG PMM, C. Pfam; PF00408; PGM PMM; I. . Pfam; PF020879; PGM PMM; I. . Pfam; PF02879; PGM PMM; II; I. Pfam; PF02879; PGM PMM; II; I. Pfam; PF02879; PGM PMM; III; I.
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Razeli C.F., Rezaian M.A.;

Razeli C.F., Rezaian M.A.;

Razeli C.F., Rezaian M.A.;

Nucleotide sequence and organization of ten open reading frames in the genome of Grapevine leafroll-associated virus 1 and identification of three subgenomic RNAS.";

of three subgenomic RNAS.";

J. Gen. Virol. 81:605-615(600).

GO: GO:0003723; F:RNA binding; IEA.

GO: GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

GO: GO:0005350; P:transcription; IEA.

GO: GO:0005350; P:viral genome replication; IEA.

InterPro; IPR001788; RNA_dep_RNApol2.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          Pyrococcus abyssi.
Archaea, Buryarchaeota, Thermococci, Thermococcales, Thermococcaceae,
Pyrococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 AA; 49786 MW; F337BA57646E7269 CRC64;
                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Greated)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNA-dependent RNA polymerase (Fragment)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00509; PGMPMM.
PROSITE; PS00710; PGM_PMM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 MEKAEKLVKDAIKKAS 450
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                                                                                        13,
24,
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        PRELIMINARY;
                                            O9UZT5;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                            01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                           Phospho-sugar mutase.
PYRAB10610 OR PAB1666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=GES / Orsay;
Heilig R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=29292;
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RESULT 6
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STRAIDERIND 2210633 / Serotype 03:K6;
STRAIDERIND 2210633 / Serotype 03:K6;
MREDLINE=222608454; PubMed=12620739;
MREDLINE=222608454; PubMed=12620739;
MREDLINE=222608464; PubMed=12620739;
MREDLINE Y., Wajima M., Nakano M., Yamashita A., Kubocta Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
EMBL, AP005088; BAC62605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                          .;
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                                                                                                                      Ouery Match 53.3%; Score 40; DB 12; Length 527; Best Local Similarity 80.0%; Pred. No. 59; Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.3%; Score 40; DB 11; Length 998; 42.9%; Pred. No. 1.2e+02; tive 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio parahaemolyticus.
Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
VCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; SECST, AMBL/GenBank/DDBJ databases.
InterPro; IPR09160; Collagen.
Pfam; PF01391; Collagen; 12.
Hypothetical protein.
NON TER 1
SEQÜENCE 998 AA; 95451 MW; 2AB4BA953B7084A6 CRC64;
                                                                                        SEQÜENCE 527 AA; 59276 MW; C445CE1169B46132 CRC64;
                                                                                                                                                                                                                                                                                                                                      01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                          PRT; 998 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Breast tumor;
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_Psvir.
Ptam; PR00978; RNA_dep_RNApol2; 1.
RNA-directed_RNA_polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           974 METIQWISRSTLKR 987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 42.9
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                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                        95 QYVVRSAİRR 104
                                                                                                                                                                                          5 OYLTRSAIRR 14
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                                                                                                                          Query Match
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamaranco S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb P.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaedacterium, Pyrococcus horikoshii OT3.",
DNA Res. 5:55-76 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                Gaps
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                                                                                         Score 40; DB 16; Length 1104; Pred. No. 1.38+02; 6; Mismatches 2; Indels 0
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Hypothetical protein; Complete proteome. SEQUENCE 1104 AA; 125574 MW; 61C89EB3AB30C5DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:000554; C:nucleus; IEA.
GO; GO:000554; C:nucleus; IEA.
GO; GO:000554; F:DAP binding; IEA.
GO; GO:000567; F:DAA binding; IEA.
GO; GO:000504; F:DAA dependent Arpase activity; IEA.
GO; GO:0006910; P:DAA replication initiation; IEA.
GO; GO:0006270; P:DAA replication initiation; IEA.
GO; GO:0006370; P:DAA replication initiation; IEA.
GO; GO:001639; P:DAA replication initiation; IEA.
GO; GO:001639; P:DAA replication initiation; IEA.
InterPro; IPR00558; Hedgehog_hint_N.
InterPro; IPR005442; INTEIN.
InterPro; IPR006141; Intein_S.
InterPro; IPR008041; Intein_S.
InterPro; IPR008045; MCM.
PFam; PF00493; MCM; I.A.
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1108 AA; 125967 MW; 92D2578B31351F75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-GAN-1999 (TrEMBLrel. 09, Last sequence update)
01-CCT-203 (TrEMBLrel. 25, Last annotation update)
1108AA long hypotherical cell division control protein.
                                                                       53.3%; Scor.
42.9%; Pred. No. 1...
... 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1108 AA.
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PRINTS; PRO1657; MCMFAMILY.
PRINTS; PRO1658; MCMFAMILY.
PRINTS; PRO1658; MCMFAMILY.
PRODOM; PD001041; MCM; 2.
SMART; SM00305; HintC; 2.
SMART; SM00305; HintC; 2.
SMART; SM00350; MCM; 2.
FIGRFAMS; TIGR01445; intein Cterm; 2.
TIGRFAMS; TIGR01445; intein Cterm; 2.
PROSITE; PS50818; INTEIN C TERE; 2.
PROSITE; PS50818; INTEIN C TERE; 2.
PROSITE; PS50818; INTEIN C TERE; 2.
PROSITE; PS50819; MCM_2; 3.
CC11 division; Complete protecome.
                                                                                                                                                                                                                                                                       853 LSKIEHITPSAVRR 866
                                                                                                                                                                                                                                1 MEKVQYLTRSAIRR 14
                                                                                         Query Match
Best Local Similarity 42.9%
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus horikoshii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=53953;
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Gaps

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"Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."; Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AJ248284; CAA49417.1; -. PIR; B75167; B75167.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PYRAB04950.
PYRAB04950 OR PAB0334.
PYROCOCCUS abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaces:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio
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0
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                52.0%; Score 39; DB 16; Length 406; 75.0%; Pred. No. 70; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.0%; Score 39; DB 2; Length 421; 50.0%; Pred. No. 73;
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Ringbauer J.A. Jr., Wall J.D.;
Ringbauer J.A. Jr., Wall J.D.;
"[Fe] hydrogenase of Desulfovibrio desulfuzicans G20.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR331719; ARXI1625.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOS GO: 0005489; Fielectron transporter activity; IEA. GOS, GO: 0005118; Fielectron transport; IEA. GOS, GO: 0005118; Fielectron transport; IEA. InterPro; IPR001450; Fe-hydrog.
InterPro; IPR004108; Fe-hydrog.
InterPro; IPR004108; Fe-hyd_1g_C.
Pfam; PF002906; Fe-hyd_1g_C.
Pfam; PF002906; Fe-hyd_1g_C.
PROSTIE; PS00139; 4FB4S FERREDOXIN; 2.
SEQUENCE Iron; Iron-sulfur.
SEQUENCE 421 AA; 46120 NW; 1116557AB0C94219 CRC64;
                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                            421 AA.
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                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fe] hydrogenase large subunit.
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Best Local Similarity 50.v.
Best Local 8; Conservative
                   Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                273 KKOVLTREAIRR 284
                                                                                                                              3 KVQYLTRSAIRR 14
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NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=876;
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01-JUN-2001
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SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / Serotype M1;
MEDLINE=21192648; PubMed=11296296;
Ferretti J.G., McShan W.M., Ajdic D.G., Savic D.G., Lyon K.,
Ferretti J.G., McShan W.M., Ajdic D.G., Savic D.G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
"Complete genome sequence of an M strain of Streptococcus pyogenes.";
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
BMBL, AR006512; ARX3342.1; ---
Hypotherical profelin; Complete proteome.
SEQUENCE 364 AA; 41754 MW; 038B8D36F4234020 CRC64;
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MEDLINE=22423660, PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beenan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Elsen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                    09-A0V9;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein SPY0549.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                   364 AA.
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                              1 MEKVOYLTRSAIRRA 15
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MEDLINE=98037514; PubMed=9371463;
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Rlocered O.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
Farmar J., Banerjee D., Fleury-Jubusson A.;
"Plateins: a novel family of signal peptide-containing articulins in
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Cycoskeletal proteins with N-terminal signal peptides: plateins in
the ciliate Euplotes define a new family of articulins.";
J. Cell Sci. 116:1291-1303(2003).
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Euplotida; Euplotidae; Euplotes.
NCBI_TaxID=5940;
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Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriacee; Methanothermobacter.
ACEL_TAXID=187420;
                                                                                                               Query Match 52.0%; Score 39; DB 17; Length 481; Best Local Similarity 50.0%; Pred. No. 84; Matches 7; Conservative 3; Mismatches 4; Indels
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GO; GO;0016020; C:membrane; IEA.
GO; GO:0005267; F:potassium channel activity; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPROU1622; K-channel_pore.
Hypothetical protein; Complete proteome.
SEQUENCE 481 AA; 55655 MW; 685FB30056A45259 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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J. Eukaryot. Microbiol. 50:19-33(2003).
EMBL: AX124991; AAM94464.1; -.
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Euplotes aediculatus
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                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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SEQUENCE FROM N.A.
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Michian D. R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J., Adredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Adredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Andredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Harison D., Haoriga L., Keagle P., Lumm W., Pothiere B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Giubon R., Jaminer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Chroniete genome sequence of Methanobacterium thermoutotrophicum RT Glathi functional analysis and comparative genomics.", J. Bacteriol. 179:7135-7155 (1997).

M. Bacteriol. 179:7135-7155 (1997).

M. Bacteriol. 179:7135-7155 (1997).

M. GO: GO:000518; F: GTP binding; IEA.

GO: GO:000518; F: Structural molecule activity; IEA.

GO: GO:000518; P: Structural molecule activity; IEA.

GO: GO:000518; P: Structural molecule activity; IEA.

GO: GO:000518; P: Structural molecule activity; IEA.

M. PROSITE: PS00228; TUBUIN. B. AUTORGG: 1.

RROSITE: PS00228; TUBUIN. B. AUTORGG: 1.

SEQUENCE 119 AA; 13045 MW; DBS119ED7630F098 CRC64;
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MEDLINE-21456156; PubMed=11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Pukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oghima T., Kikuchi H.;
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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DNA Res. 8:123-140(2001).
EMBL; APO00993; BABE5618:1;
InterPro; IFRO08301; UCP016498.
PIRSF; PIRSF016498; UCP016498; 1.
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SEQUENCE 122 AA; 14467 MW; 988A31A274842EB3 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein ST0620.
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les 6; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=33169;
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                                                        Q9HF62
Q9HF62;
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RESULT 16
Q9HF62
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MEDLINE-22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Teuruoka H., Wada T., Yamada M.,
Tabata S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradythizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005955; BAC50746.1; -.
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Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales,
Planctomycetaceae, Pirellula.
                                                                                                                                                                                                                                                                                                                    Bacteria; Protecbacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.7%; Score 38; DB 16; Length 208; 72.7%; Pred, No. 53; 1; Indels ative
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EMBL, BX294147; CAD78621.1; -.

Kinase; Transferase; Complete proteome.

SEQUENCE 211 AA; 23976 MW; 2FF54BF18F094376 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 208 AA; 22494 MW; E461C88B14783C7A CRC64;
                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Thymidine kinase Tdk (EC 2.7.1.21).
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                                                            208 AA
                                                            PRT;
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Best Local Similarity 72...
8; Conservative
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                                                            PRELIMINARY;
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                                                                                                                                                                                                                               Bll5481 protein.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=375;
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                                                                                                   289403;
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RESULT 14
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Caralles Fron Nat.

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Medium S. 192694, PubMed=11296396,

Medium S. 192694, PubMed=11296396,

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Primeaux C., Seatte S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

An an X., Clifton S., Wajar F.Z., Ren Q., Zhu H., Song L., White J.,

An an X., Clifton S.W., Roe B.A., McJaughlin R.;

An an X., Clifton S.W., Roe B.A., McJaughlin R.;

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Broc. Natl. Acad. Sci. U.S.A. 98.4658-4663(2001).

Broc. Natl. Acad. Sci. U.S.A. 98.4658-4663(2001).

Co. Go.0005737; C:cytoplasm, I.B..

GO; Go.0016491; F:coptoporphyrinogen oxidase activity; IEA.

GO; Go.0016491; F:coxidoreductase activity; IEA.

GO; GO:0016491; F:coxidoreductase activity; IEA.

GO; GO:0016491; F:coxidoreductase activity; IEA.

InterPro; IPR004559; Hemy rel.

R InterPro; IPR004559; Hemy rel.

R InterPro; IPR007197; Radical SAM;

Pfam; PF04055; Radical SAM;

R INGRAMS; TIGR00539; Hemy rel;

R TIGRPAMS; TIGR00539; Hemy rel;

R TIGRPAMS; TIGR00539; Hemy rel;

R Oxidoreductase; Complete Proteome.

SeQUENCE 376 AA, 43111 MW; 737548C68DB358E3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Wendland J., Philippsen P.;
Isolation and characterization of the Ashbya gossypii BUD3 gene.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210625; AAG41241.1; -.
                                                                                                                                                                                                                                                                        Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Ashbya.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.7%; Score 38; DB 3; Length 252; 54.5%; Pred. No. 66; 1; Indels tive 4; Mismatches 1; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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01-UN-2001 (TrEMBLrel. 17, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Putative coproporphyrinogen III oxidase (EC 1.3.3.3).
HENN OR SPY1040.
                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UJM-2003 (TrEMBLrel. 24, Last annotation update)
YC1016c (Fragment).
                                                                                                                                                                                                                                        Ashbya gossypii (Yeast) (Eremothecium gossypii)
       252 AA.
PRT;
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Best Local Similarity 54.5*
       PRELIMINARY;
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Pfam; PF04055; Radical SAM; 1.
SEQUENCE 398 AA; 45841 MW; 669A0563D1206261 CRC64;
                                   Query Match
Best Local Similarity 53.5.
And 8, Conservative
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QBK7R5;
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Q9F8B7;
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Q9F8B7
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Nakadawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Nakadawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Rawabata S., Yasunaga T., Hattori M.,
Hayashi H., Hamada S.,
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of S. pyogenes SSI-1, SF370 and MGASR332.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, APROS144, BAC64275.1;
InterPro, IPRO07197; Radical_SAM.
                                                                                                                                                                                                                                                                                                                                             STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927533; PubMed=1191108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Rapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
BMBL; AB01030; AAL97657.1; -.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0004109; F:coproporphyrinogen oxidase activity; IEA.
GO; GO:0005779; P:popphyrin biosynthesis; IEA.
InterPro; PR004559; HemN. Esl.
InterPro; IPR004559; HemN. Esl.
Fam; PF04055; Radical SAM; I.SAM.
Complete proteone: Hypothetical protein.
SEQUENCE 376 AA; 43093 MW; 7236F821EEBSEEES CRC64;
                                                                                                                                                                                                                                       Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
Putative coproporphyrinogen III oxidase.
HEMN OR SPYMI8_1022.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative coproporphyrinogen III oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 398 AA.
                                                                                                          376 AA.
                                                                                                            PRT;
102 EKIAVLQRSAVNRIS 116
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Conservative
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                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                          NCBI_TaxID=186103;
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les 8; Conserv
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NCBI_TaxID=198466;
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Matches
                                                                       RESULT 18
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SECOLOGES 15 / Serotype M3;
SETALINGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella M.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.,
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
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  Length 398;
50.7%; Score 38; DB 16; Length 39
53.3%; Pred. No. 1.1e+02;
ative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                    01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-007-2003 (TrEMBLrel. 24, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Putative coproporphyrinogen III oxidase.
HERN 08 SPYM3 0673.
Streptococcus pyogenes (serotype M3).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      emergence.";
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
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                                                                                                                                                                                                                                              PRT; 408 AA.
                                                                                                                                   124 EKIAVLORSAVNRIS 138
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                                                                                        2 EKVOYLTRSAIRRAS 16
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        Lachenauer C.S., Greti R., Michel J.L., Madoff L.C.,
"Mosaicism in the alpha-like protein genes of group B streptococci.",
Proc. Natl. Acad. Sci. U.S.A. 97:9630-9635 (2000).
-!- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bara J.J., Jin S.S.,
Fadrosh D W., Tallon LJ., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
"Oxyza sativa chromosome 3 BAC OSJNBD01079 genomic sequence.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                         EMBL, AF248038; AAG09976.1; -...
EMBL, AF248038; AAG09976.1; -...
GO, GO.0005622; C:intracellular; IEA.
GO, GO.0005700; F:transcription factor activity, IEA.
GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO, GO:0006356; P:transcription; IEA.
InterPro; IFR001034; HTH_DEOR.
Ffam; PF00455; AGOR, 1...
FROSITE; PS000894; HTH_DEOR. FAMILY; 1.
FROSITE; PS000894; HTH_DEOR. FAMILY; 1.
DNA-binding; Transcription; Transcription regulation.
SEQUENCE 578 AA; 66770 MW; CIDE74FB5943B8E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                 50.7%; Score 38; DB 2; Length 578; 50.0%; Pred. No. 1.6e+02; ative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AC137925; AAO73264.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 882 AA; 96573 MW; 5CDCB01A2569CEC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 084507 PRELIMINARY; PRT; 882 AA.
084507, 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Hypotherical protein OSJNBD0047D08.27.
MEDLINE=20402586; PubMed=10944228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 KIQFLTRQFIKQIS 319
                                                                                                                                                                                                                                                                                                                                                                                                                               3 KVQYLTRSAIRRAS 16
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Best Local Similarity 50...
Best 10 7; Conservative
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STRAIN-cv. Nipponbare;
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PRT; 1223 AA.

PRELIMINARY;

O8MMG5

RESULT 23 Q8MMG5

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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; Neguence and analysis of chromosome 2 of Dictyostellum discoideum."; Nature 418:79-85 (2002).
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                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-UN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to Homo sapiens (Human). similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BP-1;
MEDLINE=2222514; PubMed=12240834;
MEDLINE=2222514; PubMed=12240834;
Nakamara Y., Kareko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto M., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Slompte Structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: AC1165989; AAM43749.2; -
GO, GC:0005634; C:mucleus; IEA.
GO; GC:0003677; F:DNA binding; IEA.
InterPro; IPROU1605; Myb_DNA_binding.
InterPro; IPRO1673; S. mold repeat.
PERM: PF00526; S. mold repeat.
PROSTE; SR00090; MNF 3: 1.
SEQUENCE 1223 AA; I36240 MW; B7D92B2925F39C72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechococcus elongatus (Thermosynechococcus elongatus)
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NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Ferredoxin-dependent glutamate synthase.
GLSF OR TLL1368.
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EMBL; AP003373; BACC08920.1; -.

EMBL; AP003373; BCC08920.1; -.

GO; GO:000537; P:glutamate biosynthesis; IEA.

GO; GO:0006807; P:nitrogen metabolism; IEA.

InterPro; IPR002489; DUF14.

InterPro; IPR002312; Glu synthase.

InterPro; IPR006982; Glu synthace.
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Matches 8; Conservative
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InterPro; IPR006981; Glu_synth_NTN.
Pfam; PF01645; Glu_synthase; 1.
Pfam; PF04899; Glu_synth NTN; 1.
Pfam; PF04899; Glu_syn Central; 1.
Pfam; PF04493; GXGXG; T.
Complete proteome ...
SEQUENCE 1541 AA; 168017 MW; 9CB26077859306A6 CRC64;
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Hypothetical protein.
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44 KLTFLSRSAISRRAS 58
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Human pep

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Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCAZa; cardiant; cardiadomyocyte; transport peptide; penetratin; cardiac peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; recombinant peptide;

Penetratin-based recombinant phospholamban peptide, TAT-PLB.

(first entry)

29-AUG-2000

AAY71012;

AAY71012 standard; peptide; 35 AA.

RESULT 2 AAY71012

5..15 /note= "Corresponds to denatured human immunodeficiency virus (HIV) TAT protein"

Location/Qualifiers

Region

Region

Human immunodeficiency virus.

Homo sapiens

HIV; TAT protein

/note= "Corresponds to human phospholamban (PLB) amino terminal peptide"

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Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardianycoxpet; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction.
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Abu29277 Protein e
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                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                  Human Phospholamban (PLB) cargo peptide.
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ABU29277
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99US-0145883P.
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220
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Scott C,
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Example 5; Page 52; 56pp; English.
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Conservative

Best Local Similarity Matches 16; Conserv

Query Match

16;

Sequence 16 AA;

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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban [PIB] deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCAZa) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide complex comprises of transport peptide like penetratin and cargo peptide selected from muteant PIB, native PLB or antibody against blb protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCAZa interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinant peptide TAT-PLB, comprising the amino terminal end of human PLB native (HIV), TAT protein. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 75; DB 3; Length 35; 100.0%; Pred. No. 2.4e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35 AA;
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Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine

He H, Hoshijima M, Meyer M;

Dillman W, Minamisawa S, Wang Y, Silverman GJ;

Chien K, Scott C,

WPI; 2000-365393/31.

triphosphatase.

99US-0145883P.

(REGC.) UNIV CALIFORNIA.

99WO-US025692. 98US-0106718P

02-NOV-1999;

11-MAY-2000.

02-NOV-1998; 27-JUL-1999;

WO200025804-A2.

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Phospholamban, PLB; human, sarcoplasmic reticulum Ca 2+ ArFase; SERCA2a, cardiant; cardiomyocyte; transport peptide; penetratin; cards peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myccardial dysfunction; recombinant peptide; fruit fly; antennapedia; ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating cardiac diseases; e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                  /note= "Corresponds to human phospholamban (PLB) amino terminal peptide"

    .36
    Corresponds to Drosophila antennapedia (ANT)
    transport peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                         He H, Hoshijima M, Meyer M;
                                                                                                                                          Penetratin-based recombinant phospholamban peptide, PLB-ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minamisawa S,
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 52; 56pp; English.
                                                                         AAY71011 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dillman W, Minamisawa
Wang Y, Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                              99WO-US025692.
1 MEKVQYLTRSAIRRAS 16
             16 MEKVQYLTRSAIRRAS 31
                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0106718P.
                                                                                                                  29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-365393/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               triphosphatase.
                                                                                                                                                                                                                                                                                                                                                    WO200025804-A2
                                                                                                                                                                                                                                         Drosophila sp
                                                                                                                                                                                                                                                                                                                                                                                              02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1998;
                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2000
                                                                                              AAY71011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chien K,
Scott C,
                                                                                                                                                                                                                                                              Key
Region
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                                                     RESULT 3
                                                               AAY71011
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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PIB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SBRCA2a) within cardiomycytes. The peptide schered from mutant PLB, native PLB or antibody against cargo peptide schered from mutant PLB, native PLB or antibody against comminant negative inhibitor of PLB-SBRCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the contractility and reduces blood pressure this method is useful for the dysfunction. The present sequence is the penetratin-based recombinant peptide PLB-ANT, comprising the amino terminal end of human PLB native protein, attached to the 5' end of the Drosphila antennapedia (ANT) transport peptide. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the
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Sequence 36 AA;

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Gaps

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100.0%; Score 75; DB 8; Length 36; 100.0%; Pred. No. 2.5e-06; Live 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.(
Matches 16; Conservative

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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA, 2, Ca2+ Arpase of the sarco/endoplasmic reticulum) appearing as ADE45167-ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises TYT-6, AZG-9 and/or AZG-13, an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-22 and/or Phe-25 associating with an S4 binding site of the phospholamban cytosolic domain when the compound is binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzyl-23,7-bis ((IH-tetra20-15-y1) methyloxy)-4-methyl-2H-methyl-2H-1-benzopyzan-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the CA2 + -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA 2. The present sequence is the cytosolic domain of human phospholamban.
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                                                                                                                                                                                                                                                                                                                                                                                                Human; SERCA_2, phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                             Gaps
                                                                ö
                     100.0%; Score 75; DB 3; Length 36; 100.0%; Pred. No. 2.5e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovaska M, Tenhunen J, Vidgren J;
onen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                            Human SERCA_2 inhibitor phospholamban, cytosolic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 9; 65pp; English.
                                                                                                                                                                                                                                      ADE45175 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00252063.
                                                                                                    1 MEKVQYLTRSAIRRAS 16
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                                                                                                                                        1 MEKVQYLTRSAIRRAS 16
Query Match
Best Local Similarity 100...
Conservative
Trepas
                                                                                                                                                                                                                                                                                                                     (first entry)
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Yliperttula-Ikonen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-019625/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS6538022-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1999;
                                                                                                                                                                                                                                                                                                                     29-JAN-2004
                                                                                                                                                                                                                                                                               ADE45175;
                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiant.
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ADE45175
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Disclosure; Page 48; 56pp; English.
                                AAY71003 standard; protein; 52 AA.
1 MEKVOYLTRSAIRRAS 16
        1 MEKVQYLTRSAIRRAS 16
                                                  (first entry)
                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                            WPI; 2000-365393/31.
                                                                                                              Misc-difference 49
                                                                                                                                                                                                                                                                                                          Sequence 52 AA;
                                                                                                                                                                                                                    triphosphatase.
                                                                                                                           WO200025804-A2.
                                                                                            Homo sapiens.
                                                                                                                                              02-NOV-1999;
                                                                                                                                                       02-NOV-1998;
27-JUL-1999;
                                                  29-AUG-2000
                                                                                                                                     11-MAY-2000.
                                         AAY71003;
                                                                                                Synthetic
                                                                                                                                                                              Chien K,
Scott C,
                     RESULT 5
AAY71003
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Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardianycoyte; transport peptide; penetrathn; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction.
                                                                                                                                                                                                                     Human Phospholamban (PLB) wild type protein.
                                                                                                            AAY71002 standard; protein; 52 AA.
1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                    29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-1999;
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                                                                                                                                                  AAY71002;
                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                  The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum (2 2 + ATPase (SERCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising a sense mutation Val49Ala. This mutant sequence when contractility than the wild type PLB sequence
                                                                                                                                                                                                                                                                                            Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                          cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meyer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    He H, Hoshijima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Val replaced with Ala"
                                                                                                                                                                                                                                                           Human mutant phospholamban (PLB) V49A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minamisawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dillman W, Minamisawa
Wang Y, Silverman GJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0106718P.
99US-0145883P.
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/note= "Transmembrane sector made of uncharged residues responsible for stabilising the pentamer formation"

/label= Domain\_II

/label= Domain\_lb /note= "Cytoplasmic sector of the monomer"

positive charge"

1. .20 /label= Domain Ia /note= "Rich in alpha-helical confirmation with a net

Location/Qualifiers

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small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPERS (SERCAZA) within cardiomyores. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCAZA interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the dysfunction. The present amino acid sequence is the human PLB wild type apported. A potent inhibitor of SERCAZA acitivity. It primarily exists in a pentameric form. It is a mediactor in the regulation of myocardial function by catecholamines through the cAMP cascade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a method for the treatment of heart failure, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        He H, Hoshijima M, Meyer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minamisawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 47; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang Y, Silverman GJ;
                                                                                                                                                                                                                                                      98US-0106718P.
99US-0145883P.
                                                                                                                                                                       99WO-US025692.
                                                                                                                                                                                                                                                                                                                                                                                    (REGC.) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chien K, Dillman W, Scott C, Wang Y, Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-365393/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           triphosphatase.
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WO200025804-A2.
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Gaps

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100.0%; Score 75; DB 3; Length 52; 100.0%; Pred. No. 3.7e-06; Live 0; Mismatches 0; Indels

1 MEKVQYLTRSAIRRAS 16

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Best Local Similarity 100.

Query Match

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(referred to as open reading frame, ORFX, where X is 1-11431 (see Table 1 in the specification). ABN18762 to ABN7252 encode the human ORFX proteins given in ABP00010 to ABP1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a spondar associated with ORFX-associated disorder. ORFX polymorlecting a squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, infrared of interpretation, cardiovascular disorders, disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders, haemorrhage, catecathritis, neurodegenerative disorders, cholesterol ester transplantation, cardiovascular diseases, diabetes medilitus systemic transplantation, cardiovascular diseases, disorders, infectious storage disease, various immune deficiencies and disorders, infectious disease, uncommune thyroddris, mysathenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulces, for treating separative disorders, in creating or liver fibrosis, bone degenerative disorders, or protection or regeneration and treatment of lung or liver fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; open reading frame; ORFX, gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertensison; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune thyroidis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes substantially purified human proteins
                                                                                       Gaps
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                                                                                   ;
0
    Length 52;
                                                                              0; Indels
    100.0%; Score 75; DB 3; L
100.0%; Pred. No. 3.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX protein sequence SEQ ID NO:13166.
                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP06592 standard; protein; 52 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000; 2000US-0206132P. 29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                  1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                             1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-2002 (first entry)
                                                                              16; Conservative
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP06592;
                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA, 2, ADE4-1114 for, a phospholamban (PLB) protein (an inhibitor of SERCA, 2, ADE4-1173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an SI binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site of the binding site of the binding site of the binding site of moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Arg-14, a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/Or Leu-28, and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-27 and/Or Leu-28, and a hydrophobic moiety associating with an S4 binding site of the phospholamban comprises the compound is not 3-benzyl-57-bis ((1H-tetrazol-5-yl)-methyloxyl-4 methyl-2H-methyl-2H-lenzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the cac 2 + -Arasas. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse, SERCA_2, phospholamban, PLB,
Ca2+ ATPase of the sarco/endoplasmic reticulum, protein co-ordinate data,
reperfusion injury in various tissues and conditions resulting from systemic cytoKine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                            ö
                                                                                                                                                             Length 52;
                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tenhunen J, Vidgren J;
lgmann C, Lotta T, Kaivola J;
                                                                                                                                                             100.0%; Score 75; DB 5; I
100.0%; Pred. No. 3.7e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 6; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tilgmann C,
                                                                                                                                                                                                                                                                                                                                                                                                                 ADE45172 standard; protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00252063.
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                                                                                                                                                                                                                                                      1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                 1 MEKVOYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004 (first entry)
                                                                                                                                                                                                       16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yliperttula-Ikonen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-019625/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ORIN ) ORION CORP.
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                  Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pollesello P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phospholamban.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE45172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ATPase.
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                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                             ADE45172
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Fri Oct

100.0%; Pred. No. 3.7e-06;

Best Local Similarity

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ADE45170 standard; protein; 52 AA.
                                                                                                                                                     99US-00252063.
                                                                                                                                                              97US-00937117.
                                1 MEKVOYLTRSAIRRAS 16
                                        1 MEKVOYLTRSAIRRAS 16
                                                                                   29-JAN-2004 (first entry)
                                                                                                                        Oryctolagus cuniculus.
                                                                                                                                                                                     Yliperttula-Ikonen M,
                                                                                                                                                                                               WPI; 2004-019625/02.
                                                                                                                                                                       (ORIN ) ORION CORP.
    Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                      Sequence 52 AA;
                                                                                                                                                                                 Pollesello P,
                                                                                                                                                                                                                                                                                                                            phospholamban,
                                                                                                                                                              24-SEP-1997;
                                                                                                                                  US6538022-B1.
                                                                                                                                                    18-FEB-1999;
                                                                                                                                           25-MAR-2003.
                                                                          ADE45170;
                                                                                                               cardiant
                                                       RESULT 9
                                                            ADE45170
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Rattus sp.
                                                                                                                                                                                                                                                           ADE45171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                                Gaps
                                                             ö
Ouery Match
100.0%; Score 75; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovaska M, Tenhunen J, Vidgren J;
conen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rabbit SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 4; 65pp; English.
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The internation leaders to a compound within deactives, and stitute, for, a phospholamban (RLB) protein (an inhibitor of SERCA 2, and stitute, for, a phospholamban (RLB) protein (an inhibitor of SERCA 2, and stitute, for, a phospholamban creticulum) appearing as ADB45167-ADB4513. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an SI binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-12 and/or Phe-13 and/or Phe-13 and/or Phe-13 and/or Phe-13 and/or Phe-14 bencyplain administrating the novel compound to stimulate the C2 2 + -ATPage. The compound is useful for relieving the inhibitory the contains and second are deactivating the contains and second and as a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat; SERCA_2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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     Indels
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onen M, Tilgmann C, Lotta T, Kalvola J;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 5; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE45171 standard; protein; 52 AA.
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                                                                                                       1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                          1 MEKVOYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
          16; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ORIN ) ORION CORP.
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          Matches
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1 MEKVQYLTRSAIRRAS 16

Length 52;

DB 8;

Score 75;

Query Match

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1 MEKVOYLTRSAIRRAS 16
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RESULT 11

ADE45167 standard; protein; 52 AA ADE45167

ADE45167;

(first entry) 29-JAN-2004 Human SERCA 2 inhibitor phospholamban.

Human; SERCA 2; phospholamban; PLB; Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data; cardiant. 

Homo sapiens

Location/Qualifiers Key Binding-site

note= "S1 binding site residue claimed in claim 1" note= "S1 binding site residue claimed in claim 1" Binding-site

note= "S1 binding site residue claimed in claim 1" note= "S2 binding site residue claimed in claim 1" Binding-site

note= "S3 binding site residue claimed in claim 1" 'note= "S3 binding site residue claimed in claim 1" Binding-site Binding-site

note= "S4 binding site residue claimed in claim 1" note= "S3 binding site residue claimed in claim 1" Binding-site Binding-site

35 /note= "S4 binding site residue claimed in claim 1"

US6538022-B1

25-MAR-2003,

99US-00252063 18-FEB-1999; 97US-00937117.

(ORIN ) ORION CORP.

Ovaska M, Tenhunen J, Vidgren J; onen M, Tilgmann C, Lotta T, Kaivola J; Yliperttula-Ikonen M, Pollesello P,

WPI; 2004-019625/02.

phospholamban on stimulating Ca2+ New compound, useful for relieving inhibitory effects of cardiac SR Ca2+-ATPase by deactivating phospholamban and -ATPase.

Claim 1; SEQ ID NO 1; 65pp; English.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA\_2, CAS-ATPRASE of the sarcofendoplasmic reticulum) appearing as ADB45167-ADB45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an SI binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr.6, Arg-9 and/or Arg-13; an electronegative moiety associating with an SZ binding site of the phospholamban cytosolic domain when the compound is bound to it, the SZ binding site comprises Arg-14; a hydrophobic moiety associating with an SZ binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety

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associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32. and/or Phe-35. The compound is not 3-benzyl-5,7-bis ([H-tetrazol-5-yl])-methyloxyl-4-methyl-2H-methyl-2H-benzopyran-2-one. Also included are deactivating phospholamban, comprising administering the rowel compound to stimulate the Ca 2 + -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                              Length 52;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                           100.0%; Score 75; DB 8; L
100.0%; Pred. No. 3.7e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                          human phospholamban.
                                                                                                                                                                                                                                                            Local Similarity
es 16; Conserv
                                                                                                                                                                                                     Sequence 52 AA;
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                         Matches
    888888888888
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AAY71019 standard; protein; 79 AA.

1 MEKVQYLTRSAIRRAS 16

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AAY71019;

29-AUG-2000 (first entry)

H6 tagged penetratin-based recombinant protein, H6-(V49A)mutantPLB-ANT.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a, cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine.

Homo sapiens. Drosophila sp. Synthetic.

note= "Corresponds to mutant human phospholamban (PLB) Location/Qualifiers Region

"Wild type Val replaced with Ala" note= Misc-difference

protein"

"Corresponds to hexahistidine tag (H6)" ...58 /note= "C Region

63. 78 /note= "Corresponds to Drosophila antennapedia (ANT) transport peptide"

11-MAY-2000

99WO-US025692. 32-NOV-1999;

98US-0106718P. 99US-0145883P. 02-NOV-1998; 27-JUL-1999;

(REGC ) UNIV CALIFORNIA

He H, Hoshijima M, Meyer M; , Minamisawa S, Silverman GJ; Dillman W, Wang Y, Si Chien K, Scott C, 

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase

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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ Arpase (SRRCA2a) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dystunction. The present sequence is the hexahistidite (H6) tagged penetratin-based recombinant protein H6-mutantPLB-ANY, comprising the turnsport peptide attached by a hexahistidine tag. This sequence is expressed in Escherichia coli cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Corresponds to Human phospholamban (PLB) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractility; inhibitor; cardiac disease; traatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hexahistidine tagged penetratin-based recombinant protein, H6-wtPLB-ANT.
                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63. .78
/note= "Corresponds to Drosophila antennapedia (AWT)
transport peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Corresponds to hexahistidine tag (H6)"
                                                                                                                                                                                                                                                                                                                        100.0%; Score 75; DB 3; Length 79; 100.0%; Pred. No. 5.8e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71017 standard; protein; 79 AA.
Example 6; Page 56; 56pp; English.
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99US-0145883P.
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/note=
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He H, Hoshijima M, Meyer M;

Minamisawa S,

Wang Y, Silverman GJ;

WPI; 2000-365393/31.

Dillman W,

Chien K, Scott C,

(REGC ) UNIV CALIFORNIA.

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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PIB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 24 ATPaca (SERCA2A) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against CPLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure; This method is useful for the treatment of cardiac disease e.g. heart failure and mycoardial dysfunction. The present sequence is the hexahistidine (H6) tagged penetratin-based recombinant protein H6-wPLB-ANT, comprising the wild type human PLB protein and Drosophila antennapedia (ANT) transport Escherichia coli cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phospholamban, PLB, human, sarcoplasmic reticulum Ca 2+ ATPase, SERCA2a, cardiant, cardiomycorpte, transport peptide, penetratin, cargo peptide, contractilin, cardiac contractility, inhibitor, cardiac disease, treatment, heart failure, myocardial dysfunction, mutant.
         Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 75; DB 3; Length 79; 100.0%; Pred. No. 5.8e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human mutant phospholamban (PLB) S16N protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                  Example 6; Page 54-55; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY71006 standard; protein; 52 AA.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 79 AA;
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                                                                triphosphatase.
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Scott C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY71006;
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Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Disclosure; Page 49; 56pp; English.

small peptide complexes and recombinant proteins, that induces the phospholamban (FB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomycycles. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a downmant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the mutanion SerIshan. This mutant sequence when overexpressed in the transformed cardiomycoytes, shows increased contractility than the wild type PLB sequence patent discloses a method for the treatment of heart failure, using

Sequence 52 AA;

0; Gaps 96.0%; Score 72; DB 3; Length 52; 93.8%; Pred. No. 1.3e-05; 1ive 1; Mismatches 0; Indels 15; Conservative Local Similarity Query Match Matches

1 MEKVQYLTRSAIRRAS 16 ò

1 MEKVOYLTRSAIRRAN 16 d

RESULT 15 ADE45168

ADE45168 standard; protein; 52 AA. ADE45168;

29-JAN-2004 (first entry)

Pig SERCA\_2 inhibitor phospholamban.

Pig; SERCA 2; phospholamban; PLB; Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data; cardiant 

Sus sp.

US6538022-B1

25-MAR-2003.

99US-00252063, 18-FEB-1999;

97US-00937117. 24-SEP-1997;

(ORIN ) ORION CORP.

Ovaska M, Tenhunen J, Vidgren J; onen M, Tilgmann C, Lotta T, Kaivola J; Yliperttula-Ikonen M, Pollesello P,

WPI; 2004-019625/02.

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+ -ATPase.

Claim 1; SEQ ID NO 2; 65pp; English.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PL3) protein (an inhibitor of SERCA 2, Ca2+ ATPase of the sarco/endoplasmic reticulum ) appearing as ADE45167-

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ADB45173. The compound has a structure containing three of the four moieties: an electromegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it the binding site comprises Tyre, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic compain when the compound is bound, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-S5. The compound is not 3-benzyl-57-bis ([1H-tetrazol-5-yl]-methyloxyl-4 methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating chospholamban, comprising administering the novel compound to stimulate the Ca 2 + ArRese. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phospholamban.
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Sequence 52 AA;

ö Gaps ö 96.0%; Score 72; DB 8; Length 52; 93.8%; Pred. No. 1.3e-05; ive 1; Mismatches 0; Indels Conservative Local Similarity ses 15; Conserv Query Match Best Loca Matches

1 MEKVOYLTRSAIRRAS 16

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ADE45169 standard; protein; 52 AA.

29-JAN-2004 (first entry)

Dog SERCA\_2 inhibitor phospholamban.

Dog; SERCA\_2; phospholamban; PLB; Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;

Canis sp.

cardiant.

US6538022-B1.

25-MAR-2003

99US-00252063. 18-FEB-1999; 97US-00937117. 24-SEP-1997;

(ORIN ) ORION CORP.

Kaivola J; 1, Tenhunen J, Vidgren J; Tilgmann C, Lotta T, Kai Ovaska M, Pollesello P, Ovaska Yliperttula-Ikonen M, 

WPI; 2004-019625/02.

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+

Claim 1; SEQ ID NO 3; 65pp; English.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SRECA 2, Ca2+ AIPASE of the sarco/endoplasmic reticulum ) appearing as ADE45167-ADE45173. The compound has a structure containing three of the four moietles: an electronegative moiety associating with an SI binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative

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moiety associating with an S2 binding site of the phospholamban cytosolic Angeria, when the compound is bound to it, the S2 binding site comprises Arg-14; a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-35 The compound is not 3-benzyl-5,7-bis ((IH-tetrazol-5-y1)-methyl-2H-methyl-2H-benzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2 + -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiant; cardiomycoyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
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/note= "Corresponds to mutant human phospholamban (PLB)
                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penetratin-based recombinant phospholamban peptide, TAT-mutant PLB.
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                                                                                                                                                                                                                                                                         96.0%; Score 72; DB 8; Length 52; 93.8%; Pred. No. 1.3e-05; Live 1; Mismatches 0; Indels
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Scott C, Wang Y, Silverman GJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY71014 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus.
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mail peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum (a 2+ Arpase (SERCA2a) within cardiomycytes. The peptide complexes of transport peptide like penetratin and cargo peptide complex comprises of transport peptide like penetratin and cargo peptide complex comprises of transport peptide functions as a contractility and reduces blood pressure. This method is useful for the treatment of Cardiac disease e.g. heart failure and myocardial crafted rate and myocardial peptide TAT-mutant PLB, comprising the amino terminal end of human PLB mutant (Saridium) protein, attached to the 3' end of denatured human immunodeficiency virus (HTV), TAT protein Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia.
                                                                        The patent discloses a method for the treatment of heart failure, using

    20 /norresponds to mutant human phospholamban (PLB)
amino terminal peptide".

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penetratin-based recombinant phospholamban peptide, mutant PLB-ANT.
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                                                                                                                                                                                                                                                                                                                                                                                                                               94.7%; Score 71; DB 3; Length 35; 100.0%; Pred. No. 1.3e-05; ive 0; Mismatches 0; Indels
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                                  Example 5, Page 53; 56pp; English.
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Best Local Similarity
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triphosphatase
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# X # X 0.00 0.00 0.00 0.00 0.00 0.00 X &
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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces on the phospholamban (PLB) deficiency and inhibits the interaction between PLB and sercoplasmic reticulum Ca 2+ Arpase (SERCA2A) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2A interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial for the dysfunction. The present sequence is the penetratin-based recombinant opeptide, mutant PLB-ANT, comprising the amino terminal end of human PLB wutant (SerI6Glu) protein, attached to the 5' end of the Drosophila antennapedia (ANT) transport peptide. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the plasma membrane
                                                                                                       Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                         Example 5; Page 53; 56pp; English.
  Wang Y, Silverman GJ;
                                                      WPI; 2000-365393/31.
                                                                                                                                                                                   triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36 AA;
  Scott C,
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94.7%; Score 71; DB 3; Length 36; 100.0%; Pred. No. 1.3e-05; tive 0; Mismatches 0; Indels 1 MEKVQYLTRSAIRRA 15 1 MEKVQYLTRSAIRRA 15 Conservative Local Similarity les 15; Conserv Query Match à g

ABB79404 standard; peptide; 52 AA 24-JUN-2002 (first entry) ABB79404; RESULT 19

Human; phospholamban; PLB; cardiant; heart disease; gene therapy; Human phospholamban pseudophosphorylation mutant S16B PLB. cardiac function; mutant; mutein. Homo sapiens X B B B B B X B X B X B X B B B B B B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B

US2002032167-A1

Misc-difference 16

/note= "Wildtype Ser substituted by Glu"

Location/Qualifiers

14-MAR-2002.

11-SEP-2001; 2001US-00954571

11-SEP-2000; 2000US-0231821P. CHIE/) CHIEN K R.

HOSHIJMA M. (HSOH)

ROSS J. IKEDA Y. (ROSS/) Chien KR, Hoshijma M, Ross J,

Ikeda Y;

WPI; 2002-361185/39 

Delivering a dose of a gene expression cassette in a fluid selectively to heart for sustained expression, useful for improving or enhancing cardiac function, by employing a viral vector together with a vascular permeablizing agent.

Example 6; Fig 1; 12pp; English

The invention relates to delivering a therapeutic dose of a gene expression cassette in a fluid selectively to heart for sustained expression, comprising employing a viral vector together with a vascular permeabilising agent. The method is useful for gene therapy delivering genes for improving or enhancing cardiac function, particularly in hamster models of heart disease. The present sequence is that of a pseudophosphorylation mutant of phospholamban (SIGEPLB). This point mutant is among a number of dominant negative mutants identified and characterised in WOOO/25804 and used in the method of the present invention

Sequence 52 AA;

Gaps °, 94.7%; Score 71; DB 5; Length 52; 100.0%; Pred. No. 2e-05; ive 0; Mismatches 0; Indels 15; Conservative Query Match Best Local Similarity Matches

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RESULT 20 ADE45173

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0; Gaps

ADE45173 standard; protein; 52 AA.

ADE45173;

(first entry) 29-JAN-2004 Chicken SERCA\_2 inhibitor phospholamban.

Chicken; SERCA\_2; phospholamban; PLB; Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data; cardiant.

Gallus sp.

US6538022-B1

25-MAR-2003.

18-FEB-1999;

99US-00252063. 97US-00937117. 24-SEP-1997;

(ORIN ) ORION CORP.

M, Tenhunen J, Vidgren J; Tilgmann C, Lotta T, Kaivola J; Ovaska M, Yliperttula-ikonen M, Pollesello P,

WPI; 2004-019625/02.

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+ -ATPase. 

Claim 1; SEQ ID NO 7; 65pp; English.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, Ca2+ ATPage of the sarco/endoplasmic reticulum ) appearing as ADB45167-ADB45173. The compound has a structure containing these of the four molecies: an electronegative molecy associating with an S1 binding site

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of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative moiety associating with an $2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the $2 binding site comprises Arg-14; a hydrophobic moiety associating with an $3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an $3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is not 3-benzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2 + -Arpsase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phospholamban; PLB; human, sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a, cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractility; inhibitor; cardiac disease; mutant; transment; heart failure; myccardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Corresponds to mutant human phospholamban (PLB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H6 tagged penetratin-based recombinant protein, H6-(S16E) mutantPLB-ANT
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                                                                                                                                                                                                                                                                                                             94.7%; Score 71; DB 8; Length 52; 87.5%; Pred. No. 2e-05; 0; Indels ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY71018 standard; protein; 79 AA.
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99US-0145883P.
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les 14; Conservative
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                                                                                                                                                                                                                                                                                   Sequence 52 AA;
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                                                                                                                                                                                                                                             phospholamban.
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Synthetic.
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Meyer M;

Hoshijima M,

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Dillman W, Minamisawa S, Wang Y, Silverman GJ;

Chien K, Scott C,

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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 24 ATPaca (SERCACA) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against DLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCACA interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial cysfunction. The present sequence is the hexabisticine (H6) tagged penetratin-based recombinant protein H6-mutantPLB-NNT, comprising the human mutant (SerlGGlu) PLB protein and Drosophila antennapedia (ANT) expressed in Escherichia coli cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomycoytre; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.
                             Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Scott C, Wang Y, Silverman GJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human mutant phospholamban (PLB) R14E protein.
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                                                                                                                          Example 6; Page 55; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71005 standard; protein; 52 AA.
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Best Local Similarity 100.
Matches 15; Conservative
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WPI; 2000-365393/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 79 AA;
                                                                                         triphosphatase.
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Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase

Disclosure, Page 48-49; 56pp; English.

small peptide complexes and recombinant proteins, that induces by phospholamban (PB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum G2 + ArBase (SBRCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide sclerced from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SBRCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein. comprising a sense mutafich Argiddium, ownershing and myocardial overexpressed in the transformed cardiomyocytes, shows increased contractility than the wild type PLB sequence The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces

Sequence 52 AA;

Gaps . 93.3%; Score 70; DB 3; Length 52; 93.8%; Pred. No. 3e-05; 1; Indels cive 0; Mismatches 1; Indels 1 MEKVOYLTRSAIRRAS 16 1 MEKVOYLTRSAIREAS 16 Query Match Best Local Similarity 93.8 Matches 15, Conservative a

ö

RESULT 23

AAY71004 standard; protein; 52 AA. AAY71004;

29-AUG-2000 (first entry) 

Human mutant phospholamban (PLB) E2A protein.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomycoytre; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.

sapiens. Synthetic

/note= "Wild type Glu replaced with Ala" Location/Qualifiers Misc-difference 2

WO200025804-A2

11-MAY-2000.

99WO-US025692 02-NOV-1999;

98US-0106718P 99US-0145883P 02-NOV-1998; 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

Meyer M; Hoshijima M, не н, Minamisawa S, Wang Y, Silverman GJ Dillman W, Chien K, Scott C,

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

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small peptide complexes and recombinant proteins, that induces the phospholauban (PbB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca + ATPase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, mative PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the mutation Glu2Ala. This mutant sequence when contractility than the wild type PLB sequence
                                                                                                                                                                        The patent discloses a method for the treatment of heart failure, using
comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.
                                                                                                                        Disclosure, Page 48; 56pp; English.
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Sequence 52 AA;

.. 0 Gaps ; 0 92.0%; Score 69; DB 3; Length 52; 93.8%; Pred. No. 4.6e-05; ive 0; Mismatches 1; Indels 1 MEKVQYLTRSAIRRAS 16 1 MAKVOYLTRSAIRRAS 16 Local Similarity 93,8 es 15; Conservative Query Match Matches q

RESULT 24

AAY71007 standard; protein; 52 AA.

29-AUG-2000 (first entry)

Human mutant phospholamban (PLB) K3E/R14E protein.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.

sapiens.

Synthetic

'note= "Wild type Lys replaced with Glu" /note= "Wild type Arg replaced with Glu" Location/Qualifiers Misc-difference 14 Misc-difference 3

WO200025804-A2

11-MAY-2000

99WO-US025692. 02-NOV-1999;

99US-0145883P. 02-NOV-1998; 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

Hoshijima M, He H, ທັ Dillman W, Minamisawa Wang Y, Silverman GJ; Chien K, Scott C, 

WPI; 2000-365393/31

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine riphosphatase.

Disclosure; Page 49; 56pp; English.

small peptide complexes and recombinant proteins, that induces the phospholamban (PDB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Cat ATPASS (SERCAS) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin) Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2 interaction, enhances cardiac confractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein. Comprising the double mutation Lysallu and Argisclu. This mutant sequence, when overexpressed in the transformed cardiomycoytes, shows increased contractility than the wild type PLB sequence patent discloses a method for the treatment of heart failure, using

Sequence 52 AA;

Gaps ; 0 88.0%; Score 66; DB 3; Length 52; 87.5%; Pred. No. 0.00016; Live 1; Mismatches 1; Indels 1 MEKVOYLTRSAIRRAS 16 1 MEEVOYLTRSAIREAS 16 Query Match Best Local Similarity 87.5% Matches 14, Conservative ò g

RESULT 25

ADC87928 standard, protein; 116 AA. ADC87928;

Ribosomal protein similar to FCWP1 #144. 01-JAN-2004 (first entry) 

Antifungal protein, ribosomal protein; FCWP1; AlyAFP; plant fungal infection; Alternaria; Ascochyta; Borrytis; Cercospora; Colletcrichum; Diplodia; Pusarium; Gaeumanomyces; Helminthosporium; Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma; Phoma; Phytophthora; Phytophthora; Phytophthora; Phythium; Phytophthora; Phythium; Rhizoctonia; Scerotium; Sclerotinia; Septoria; Thielaviopsis; Venturia; Verticillium.

Unidentified

US6573361-B1.

03-JUN-2003.

07-DEC-2000; 2000US-00732210.

99US-0169340P. 99US-0169513P. 07-DEC-1999; 07-DEC-1999; (MONS ) MONSANTO TECHNOLOGY LLC.

Liang J,

Bunkers GJ,

Wu YS;

Mittanck CA, Seale JW,

Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful for controlling fungal infections in plants. WPI; 2003-754558/71.

Example 21; SEQ ID NO 181; 27pp; English.

The invention relates to an isolated antifungal ribosomal protein from

custium culmorum, FCWP1. Also included is a fusion protein between the signal peptide of the antifungal protein AlyAPP From AlySama and FCWP1, concoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are useful for controlling fungal infections in plants, such as those caused by Alternaria (e.g. Ascochyra pisi). Botrytis (e.g. Botrytis cinera), accompyra (e.g. Ascochyra pisi), botrytis (e.g. Botrytis cinera), collectrichum (e.g. Ascochyra pisi). Botrytis (e.g. Botrytis cinera), collectrichum (e.g. Celrospora azaa-maydis), collectrichum (e.g. Celrospora azaa-maydis), collectrichum (e.g. Pusatium culmorum, Fusatium acyporum, plantim roseum), Diplodia maydis), bearium roseum), Gaeumanomyces (e.g. Gaemanomyces (e.g. Gaemanomyces (e.g. Haminthosporium carbonum, Helminthosporium (e.g. Helminthosporium ucronum, Helminthosporium (e.g. Helminthosporium (e.g. Phrophhora parasibutes), Nectria (e.g. Maccophaerala figialas), Nectria (e.g. Hancophaerala figialas), Nectria (e.g. Phrophhora collamonamomyces (e.g. Phrophhora parasibutes), Peronospora acatorum, Phycophhora acatorum, Phycophhora acatorum, Phycophhora acatorum, Phycophhora phaseoli, Phycophhora parasitica, Phytophhora phaseoli, Phycophhora acatorum, Phycophhora phaseoli, Phycophhora parasitica, Phytophhora phaseoli, Phycophhora megasperma f.g. buccinia scencium, Phytophhora phaseoli, Phytophhora parasitica, Phytophhora phaseoli, Phytophhora parasitica, Phytophhora phaseoli, Phytophhora parasitica, Phytophhora phaseoli, Phytophhora parasitica, Phytophhora phaseoli, Phytophhora parasitica, Phytophhora phaseoli, Phytophhora megasperma f.g. buccinia accordina phantiermanum, Phytophhora phaseoli, Phytophhora phaseoli, Phytophora phaseoli, Phytophora phaseoli, Phytophora phaseoli, Phyt ö Gaps . 0 54.7%; Score 41; DB 7; Length 116; 46.7%; Pred. No. 14; 3; Indels iive 5; Mismatches 3; Indels Search completed: October 1, 2004, 12:13:15 Job time : 63.2 secs 1 MEKVQYLTRSAIRRA 15 Conservative Local Similarity les 7; Conserv Sequence 116 AA; Query Match Matches à

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0; Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            1 MEKVQYLTRSAIRRAS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Marti
APPLICANT: Tenhumen, Jukka
APPLICANT: Tenhumen, Jukka
APPLICANT: Tilgment, Jukka
APPLICANT: Tilgment, Carola
APPLICANT: Tilgment, Carola
APPLICANT: Tilgment, Carola
APPLICANT: Tilgment, Carola
APPLICANT: Maivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1997-02-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEO ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Pollseello, Piero
APPLICANT: Pollseello, Martki
APPLICANT: Tenhunen, Jukka
APPLICANT: Tenhunen, Jukka
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Juka
APPLICANT: Tilgann, Carola
APPLICANT: Tilgann, Carola
APPLICANT: Lotta, Timo
APPLICANT: Corta, Timo
APPLICANT: Lotta, Timo
APPLICANT: Candrage (Phospholamban Inhibitors)
FILE REFERENCE: 1102.025001
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
SEARLIER APPLICATION NUMBER: 08/937,117
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT TO NO. COT T
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                                                                                                   ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09252063
Patent No. 6538022
GENERAL INFORMATION:
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US-09-252-063-1
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Matches 16; Conserv
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LENGIH: 36
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LENGTH: 52
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APPLICANT: Poliseallo, Piero
APPLICANT: Poliseallo, Piero
APPLICANT: Poliseallo, Marti
APPLICANT: Poliseallo, Marti
APPLICANT: Tenhunen, Jukka
APPLICANT: Videren, Jukka
APPLICANT: Vilertula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Juha
APPLICANT: Lotta, Juha
APPLICANT: Lotta, Juha
TITLE OF INVENTION: Ca-ArPase (Phospholamban Inhibitors)
FILE REPERENCE: 1102.0250001
FILE REPERENCE: 1102.0250001
CURRENT FILING DATE: 1999-02-18
BARLIER APPLICATION NUMBER: 08/937,117
BARLIER APPLICATION NUMBER: 08/937,117
BARLIER PILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 52
                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Piero
APPLICANT: Tenhumen, Jukka
APPLICANT: Tenhumen, Jukka
APPLICANT: Tenhumen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Tilgann, Carola
APPLICANT: Tilgann, Carola
APPLICANT: Tilgann, Carola
APPLICANT: Tilgann, Campounds for Deactivating Phospholamban Function on ITILE OF INVENTION: Ca-APPRES (Phospholamban Inhibitors)
ITILE OF INVENTION: Ca-APPRES (Phospholamban Inhibitors)
ITILE OF INVENTION: Ca-APPRES (18/09/252,063)
ITILE APPLICATION NUMBER: 18/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER FILING DATE: 1999-02-18
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
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                                                                                                         US-09-252-063-4
; Sequence 4, Application US/09252063
; Patent No. 6538022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-252-063-4
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1 MEKVOYLTRSAIRRAS 16
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US-09-252-063-5
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LENGTH: 52
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US-09-252-063-6

Sequence 6, Application US/09252063

Sequence 6, Application US/09252063

SENEMAL INFORMATION:
APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Dikka
APPLICANT: Tethunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Tilgmann, Carola
APPLICANT: Aligmann, Carola
APPLICANT: Arivola, Juha
APPLICANT: Kaivola, Juha
APPLICANT: Kaivola, Juha
APPLICANT: Kaivola, Juha
APPLICANT: Lotta, Timo
APPLICANT: Kaivola, Juha
APPLICANT: Raivola, Juha
APPLICANT: Raivola, Juha
APPLICANT: Raivola, Juha
APPLICANT: NOWBER: US/09/252,063
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT APPLICATION NUMBER: 1999-02-18
BARLIER APPLICATION NUMBER: 08/937,117
SEALIER PILING DATE: 1999-02-18
SEALIER PILING DATE: 1999-02-18
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                   0; Gaps
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Query Match
100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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Sequence 15, Application US/09549872B

GENERAL INFORMATION

APPLICANT: Groenen, Jose

APPLICANT: Groenen, Jose

APPLICANT: Beggert, Thierry

TITLE OF INVENTION: COMPOUND SCREENING METHODS

FILE REFERENCE: D00590/70006 (JRV/RE)

CURRENT APPLICATION NUMBER: US/09/549,872B

CURRENT FILING DATE: 1999-04-14

PRIOR APPLICATION NUMBER: US 60/129,596

PRIOR APPLICATION NUMBER: US 60/129,596

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 39

SEQ ID NO 15

LENGTH: 52
                                                                                                                  1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                         1 MEKVOYLTRSAIRRAS 16
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CRGANISM: Homo sapiens
US-09-549-872B-15
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Best Local Similarity
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US-09-549-872B-15
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| Fatent No. 2018/02|
| Fatent No. 2018/02|
| GENERAL INFORMATION:
| APPLICANT: Pollesello, Piero
| APPLICANT: Tenhunen, Jukka
| APPLICANT: Tenhunen, Jukka
| APPLICANT: Tenhunen, Jukka
| APPLICANT: Tilgmann, Carola
| APPLICANT: Tilgmann, Carola
| APPLICANT: Tilgmann, Carola
| APPLICANT: Tilgmann, Carola
| APPLICANT: Tilgmann, Carola
| APPLICANT: Asivola, Juha
| APPLICANT: Asivola, Juha
| TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
| FILE REPERBANCE: 1102.0250001
| CURRENT APPLICATION NUMBER: US/09/252,063
| CURRENT FILING DATE: 1999-02-18
| EARLIER FILING DATE: 1999-02-24
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 3
| LENGTH: 52
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**APPLICANT: Pollegello, Piero
**APPLICANT: Pollegello, Dikka
**APPLICANT: Tenhunen, Unkka
**APPLICANT: Tenhunen, Unkka
**APPLICANT: Vilgerttula-Ikonen, Marjo
**APPLICANT: Vilgerttula-Ikonen, Marjo
**APPLICANT: Tilgenan, Tanda
**APPLICANT: Tilgenan, Carola
**APPLICANT: Cotta, Timo
**APPLICANT: Congounds for Deactivating Phospholamban Function on
**TITLE OF INVENTION: Ca-APPRES (Phospholamban Inhibitors)
**TITLE OF INVENTION: Ca-APPRES (Phospholamban Inhibitors)
**TITLE OF INVENTION: Ca-APPRES (Phospholamban Inhibitors)
**TITLE OF INVENTION: US/09/252,063
**CURRENT FILING DATE: 1999-02-18
**EARLIER PILING DATE: 1997-09-24
**NUMBER OF SEQ ID NOS: 10
**SOFTWARE: PatentIn Ver. 2.0
**SOFTWARE: PatentIn Ver. 2.0
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                                                               Gaps
Query Match 100.0%; Score 75; DB 4; Length 52; Best Local Similarity 100.0%; Pred. No. 3e-07; Matches 16; Conservative 0; Mismatches 0; Indels
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US-09-252-063-2
IS-09-252-063-2
Factoric US/09252063
Factor No. 6538022
GENERAL INFORMATION:
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; Sequence 3, Application US/09252063
; Patent No. 6538022
                                                                                                                      1 MEKVQYLTRSAIRRAS 16
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Matches 15; Conservative
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ORGANISM: Canis sp.
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LENGTH: 52
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US-09-252-991A-18000
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APPLICANT: Polleseallo, Piero
APPLICANT: Tenhunen, Jukka
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Juka
APPLICANT: Vidgren, Juha
APPLICANT: Alignann, Carola
APPLICANT: Lotta, Timo
APPLICANT: Congounds for Deactivating Phospholamban Function on TITLE OF INVENTION: Camplese (Phospholamban Inhibitors)
TITLE OF INVENTION: Ca-APPese (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER FILING DATE: 1999-02-18
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 10
                                                   0; Gaps
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96.0%; Score 72; DB 4; Length 52; 93.8%; Pred. No. 1.1e-06; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Zwaal, Richard
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70088 (URV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURKENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-01
PRIOR PLING DATE: 1999-06-01
SOFTWARE: PALENTIN NUMBER: GB 9912736.7
SOFTWARE: PALENTIN VOR: 30
SOFTWARE: PALENTIN VOR: 2.0
                                                                                                                                                                                                                                        US-09-549-872B-14; Sequence 14, Application US/09549872B; Patent No. 6540996
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Patent No. 6538022
                                                                                               1 MEKVOYLTRSAIRRAS 16
                                                                                                                                           1 MDKVQYLTRSAIRRAS 16
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Best Local Similarity 93.8*
Matches 15, Conservative
                                                 15; Conservative
  Query Match
Best Local Similarity
Matches 15; Conserva
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APPLICATION: MAIC O'S RUBenfield et al.
APPLICATION: MAIC O'S RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: APRUGANCS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERSENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/0074,788
PRIOR APPLICATION NUMBER: US/0074,190
PRIOR FILING DATE: 1998-07-27
NUMBER O'S EQUID NOS: 33142
SEQ ID NO 18000
LENGTH: 631
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                                                                         Gaps
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APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Way Younle S.
TILLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21 (1503) 8 (9)/732,210
CURRENT APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
SEQ ID NO. 181
LENGTH: 116
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49.3%; Score 37; DB 4; Length 631;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 7; Conservative 4; Mismatches 3; Indels
                   94.7%; Score 71; DB 4; Length 52; 87.5%; Pred. No. 1.7e-06; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 'Sequence 18000, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                          ; Sequence 181, Application US/09732210; Patent No. 6573361; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT , ORGANISM: Streptomyces coelicolor US-09-732-210-181
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                                                                                                                       1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                  1 MEKVQYLTRSAIRRA 15
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Query Match
Best Local Similarity 87.5%
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Best Local Similarity 46.73
Matches 7; Conservative
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Sequence 24791 Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
PATENCE OF INVENTION:
PAPPLICANT:
MARC J. Rubenfield et al.
TITLE OF INVENTION:
MICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24791
LENGTH: 765
                                                                                                                                                                                             Query Match 48.0%; Score 36; DB 4; Length 686; Best Local Similarity 77.8%; Pred. No. 1.38+02; Matches 7; Conservative 1; Mismatches 1; Indels
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48.0%; Score 36; DB 4; Length 765;
Best Local Similarity. 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,983
FILING DATE: Concurrently herewith
CLASSIFICATION: 424
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Patent No. 5854067
GENERATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: for Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                     ORGANISM: Pseudomonas aeruginosa
1998-07-27
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                     NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 19332; LENGTH: 686
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                                                                                                                                                                                                                                                                                                                                           522 VQYLTRSGL 530
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PRIOR FILING DATE:
                                                                                                                                                 US-09-252-991A-19332
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US-09-252-991A-24791
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                                                                                               TYPE: PRT
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Patent No. 6551795
GENERAL INFORMATION
FOR A PARTICULAR

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
                                                      Patent No. 6610836
GENERAL INFORMATION
FATTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-29

FRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 48.0%; Score 36; DB 4; Length 98; Best Local Similarity 58.3%; Pred. No. 15; Matches 7; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE; PRT ORGANISM: Klebsiella pneumoniae
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51 KPQHLTRSGMRK 62
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US-09-489-039A-11071
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                   RESULT 13
US-09-489-039A-7319
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Sequence 28352, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION
ABRICANT: MARCA INCLUDED AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196.136
CURRENT APPLICATION NUMBER: US/09/2219
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO. 28362
LENGTH: 210
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; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: LYND DOUGETE-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTERCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
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46.7%; Pred. No. 54;
tive 3; Mismatches 5; Indels
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Best Local Similarity 53.8%; Pred. No. 54;
Matches 7; Conservative 3; Mismatches 3; Indels
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; Sequence 5136, Application US/09134001C
; Patent No. 6380370
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5136
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
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Matches 7, Conservative
                                     RESULT 19
US-09-252-991A-28362
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US-09-134-000C-6395
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Pred. No. 1.8e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                     Length 924;
                                                                                                                                                                                                                                                                                                                                                Query Match 48.0%; Score 36; DB 2; Length 924 Best Local Similarity 61.5%; Pred. No. 1.86+02; Matches 8; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Petcentur Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/588,976

FILING DATE: Concurrently herewith

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-757
                                                             UTSD:424/FUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/08588976
Patent No. 5891717
              NAME: PUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REPRENCE DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 18:
SEGURICE CHARACTERISTICS:
LENGTH: 924 amino acids
                                                                                                                                                TELEX: n/a
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     638 ODVVYLLREAIRR 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EKVQYLTRSAIRR 14
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US-08-588-976-18
                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
US-08-588-983-18
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638 QDVVYLLREAIRR 650

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US-09-620-461-14

i Sequence 14, Application US/09620461

parent No. 6635750

GENERAL INFORMATION:

APPLICANT: Coyle, Anthony J.

APPLICANT: Coyle, Anthony J.

APPLICANT: Fraser, Christopher C.

APPLICANT: Fraser, Christopher C.

APPLICANT: Fraser, Christopher C.

APPLICANT: Fraser, Christopher C.

TITLE OF INVENTION: 87-412 Molecules, No. 6635750e1 Members of the B7

TITLE OF INVENTION: Family and Uses Thereof

FILE REFERENCE: 5800-149

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 29

NUMBER OF SEQ ID NOS: 29

CONTRARER FRASEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09910174B

### Sequence 14, Application US/09910174B

### Sequence 14, Application US/09910174B

### Sequence 14, Application US/09910174B

### SPECIAL INFORMATION:
### APPLICANT: COYIE, Anthony J.

### APPLICANT: Manning, Stephen

### TITLE OF INVENTION: B-H-12 Molecules, No. 6630575el Members of the B7

### TITLE OF INVENTION: B-H-12 Molecules, No. 6630575el Members of the B7

### TITLE OF INVENTION: Family and Uses Thereof

### TITLE OF INVENTION: Family and Uses Thereof

### FILE OF INVENTION: B-M-12 Molecules, No. 6630575el Members of the B7

### TITLE OF INVENTION: B-M-12 Molecules, No. 6630575el Members of the B7

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### TITLE OF INVENTION: B-M-12 Molecules, No. 6630575el Members of the B7

### TITLE OF INVENTION: B-M-12 Molecules, No. 6630575el Members of the B7

### TITLE OF INVENTION: B-M-12 Molecules, No. 6630575el Members of the B7

### TITLE OF INVENTION: B-M-12 Molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
46.7%; Score 35; DB 4; Length 216;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 4; Indels
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CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: Patentin version 3.1 SEQ ID NO 6395 LENGTH: 216
                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6395
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 KKIQYLTR 320
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CORGANISM: Homo sapiens
US-09-620-461-14
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LENGTH: 357
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LENGTH: 357
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Sequence 4, Application US/09277262
| Sequence 4, Application US/09277262
| Parent No. 6395482
| General INFORMATION:
| APPLICANT: Karayiorgou, Maria
| APPLICANT: Gogos, Joseph A |
| TITLE OF INVENTION: WETHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE |
| TITLE OF INVENTION: THERETO |
| TITLE OF INVENTION: THERETO |
| TITLE OF INVENTION: THERETO |
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| TITLE OF INVENTION: THERETO |
| TITLE OF INVENTION: THERETO |
| TITLE OF INVENTION WINDER: US/09/277,262 |
| CURRENT PELING DATE: 1999-03-26 |
| EARLIER APPLICATION NUMBER: 09/229,530 |
| EARLIER APPLICATION NUMBER: 09/229,530 |
| EARLIER PETERORY |
| NUMBER OF SEQ ID NOS: 9 |
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1 Sequence 2, Application US/09277262

2 Sequence 2, Application US/09277262

3 Sequence 2, Application US/09277262

3 Sequence 2, Application US/09277262

4 Settent No. 6399403

5 SEQUENCE INFORMATION:

4 APPLICANT: Garayiorgou, Maria

5 APPLICANT: Garayiorgou, Maria

5 APPLICANT: Garayiorgou, Maria

6 TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE

7 TITLE OF INVENTION: THERETO

7 TITLE OF INVENTION: THERETO

7 TITLE OF INVENTION: THERETO

7 TITLE OF INVENTION NUMBER: US/09/277,262

7 CURRENT APPLICATION NUMBER: US/09/277,262

7 SEALLER APPLICATION NUMBER: 09/229,530

7 SARLIER FILING DATE: 1999-01-13

7 NUMBER OF SEQ ID NOS: 9

7 SEQ ID NO 2

7 LENGTH: 516
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Query Match 46.7%; Score 35; DB 4; Length 357; Best Local Similarity 75.0%; Pred. No. 97; Matches 6; Conservative 2; Mismatches 0; Indels
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43.8%; Pred. No. 1.4e+02;
tive 4; Mismatches 5; Indels
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46.7%; Score 35; DB 4; Length 516
Best Local Similarity 43.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 5; Indels
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Best Local Similarity 43.88
Matches 7; Conservative
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; LENGTH: 497
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-277-262-4
                                                                                                                                                                                                                                                                                                        313 KKIQYLTR 320
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, ORGANISM: Homo sapiens
US-09-277-262-2
                                                                                                                                                                                                            2 EKVQYLTR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 24
US-09-277-262-4
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Fri Oct

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Sequence 201301, Sequence 13984, A Sequence 13981, Sequence 13981, Sequence 170920, Sequence 170920, Sequence 170320, Sequence 5733, Ap Sequence 52593, Ap Sequence 171415, Application of the sequence 19521, Sequence 19523, Application of the sequence 19523, Application of the sequence 19523, Application of the sequence 19523, Application of the sequence 19523, Application of the sequence 19523, Application of the sequence 19523, Application of the sequence 19523, Application of the sequence 19523, Sequence 19522, Sequence 198334, Sequence 128334, Sequence 128334, Sequence 128334, Sequence 128334, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 128339, Sequence 12833
                                                    Sequence 18, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 238702,
Sequence 46161, A
Sequence 10177, A
Sequence 21630, A
Sequence 21630, A
Sequence 20314, A
Sequence 20314, A
Sequence 20314, A
Sequence 53984, A
Sequence 53984, A
Sequence 53984, A
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Sequence 413, App
Sequence 40542, A
Sequence 41598, A
Sequence 1012, Ap
Sequence 14511,
Sequence 145511,
                        Sequence
Sequence
6 US-10-705-791-13

6 US-10-705-791-13

6 US-10-705-791-12

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                                                                                                                     October 1, 2004, 12:18:23 ; Search time 63.4 Seconds (without alignments) 81.211 Million cell updates/sec
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US-10-705-791-11
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Match Length
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APPLICANT: He, Huaping
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APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Mang, Vibin
APPLICANT: Soct, Cristopher
APPLICANT: Sliverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-863025
CURRENT APPLICATION NUMBER: 60/106,718
FRIOR PELING DATE: 1999-11-02
FRIOR PELING DATE: 1999-11-02
FRIOR FILING DATE: 1999-11-02
FRIOR PELING DATE: 1999-11-02
FRIOR FILING DATE: 1999-11-02
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TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT PILING DATE: 2003-11-10
PRIOR FILING DATE: 1998-11-02
PRIOR PLING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: RECHING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: BECENTIN VERSION 3.2
SOFTWARE: SECOLULY OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 10, Application US/10705791; Publication No. US20040121942A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 Application US/09954571
Publication No. US20200032167A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
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Best Local Similarity 100.
Matches 16; Conservative
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ORGANISM: Homo sapiens
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US-10-705-791-10
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US-10-705-791-10
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APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Mayor, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibhn
APPLICANT: Wang, Yibhn
APPLICANT: Wang, Yibhn
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: OF CARDIAC DISBASE
FILLE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: 105/10/705,791
FILLE REPERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: 60/106,718
PRIOR PELING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SSOFWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 16
                                                                                      Sequence 61911, A Sequence 103091, Sequence 442, App Sequence 442, App Sequence 71171, App Sequence 57201, A
                                                                                                                                                                                                                                                                                                                                               Sequence 164, App
Sequence 2255, Ap
Sequence 52269, A
                       Sequence 152503,
                                                   Sequence 147002,
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           ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-10-05-791-8
Sequence 8, Application US/10705791
Sequence 9, Publication No. US20040121942A1
GENERAL INFORMATION:
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Hoshijima, Masahiko
Meyer, Markus
Scott, Christopher
Wang, Yibin
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US-10-705-791-8
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US-10-705-791-11
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Best Local 9
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US-10-408-765A-478
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100.0%; Score 75; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps
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APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ross, John
APPLICANT: Reas, John
TITLE APPLICANT: TREAD, YASHAILO
TITLE OF INVENTION: HIGH FFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: 00/09/954,571
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR RILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Version 3.2
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 75; DB 12; Length 52; Best Local Similarity 100.0%; Pred. No. 1.9e-06; Matches 16; Conservative 0; Mismatches 0; Indels
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Sequence 5, Application US/09954571

Sequence 5, Application US/09954571

GENERAL INFORMATION:

APPLICANT: Chien, Kenneth R

APPLICANT: Hoshijima, Masahiko

APPLICANT: Ross, Yasuhiko

APPLICANT: Reda, Yasuhiko

TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER

FILE REFERENCE: 6627-PA0123

CURRENT APPLICATION NUMBER: US/09/954,571

CURRENT PILING DATE: 2000-11

PRIOR APPLICATION NUMBER: 2000-11

PRIOR FILING DATE: 2000-11-09
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Sequence 4, Application US/09954571

Publication No. US2020032167A1

GENERAL INFORMATION:

APPLICANT: Chien, Kenneth R

APPLICANT: Ross, John

APPLICANT: Ikeds, Vasuhico

TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER

FILE REPERENCE: 6627-FA0123

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: 06/231,821

PRIOR FILING DATE: 2001-109-11

PRIOR FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.2
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US-09-954-571-2
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SEQ ID NO 4
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APPLICANT: Glason, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THE RAPEUTIC INTERVENTION
TITLE REPERSENCE: 660089465
CURRENT FILING DATE: 2003-04-04
CURRENT FILING DATE: 2003-04-04
SUUMBER OF SEQ ID NOS: 3077
SUUMBER OF SEQ ID NOS: 3077
                                                                                                                                                                                                                                    Query Match 100.0%; Score 75; DB 12; Length 52; Best Local Similarity 100.0%; Pred. No. 1.9e-06; Matches 16; Conservative 0; Mismatches 0; Indels
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Sequence 15, Application US/10371101
PUBLICATION NO. US20030149995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: DOSSO.70035.US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
SPRIOR FILING DATE: 1999-06-01
SPRIOR FILING DATE: 1999-06-01
SPRIOR FILING DATE: 2090-06-01
SPRIOR FILING DATE: 2090-06-01
SPRIOR FILING DATE: 2090-06-01
SPRIOR FILING DATE: 200
SEQ ID NOS: 39
SOFTWARE: PALENTIN VONCEEN
SEQ ID NO 15
LENGTH: 52
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                                                                                                                ) TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-954-571-5
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                           1 MEKVOYLTRSAIRRAS 16
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Matches 16; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Mang, Vibin
APPLICANT: Soct, Christopher
APPLICANT: Siverana, Gorgg U.
TILLE OF INVENTION: GTORDIAC DISEASE
FILE REPREBRUE: 662-Pago25
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: 60/106,718
FRIOR PEPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
SEQ ID NO 17
LENGTH: 79
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Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Dillmann, Wolfgang
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR PPLICATION NUMBER: 66/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFWARE: Patent In version 3.2
LENGTH: 52
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Matches 16; Conservative
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ORGANISM: Escherichia coli
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ORGANISM: Homo sapiens
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APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Gott, Markus
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Xibin
APPLICANTON: WETHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT;
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT FILING DATE: 2003-11-02
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER: OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
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APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Mashus
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Wang, Xibin
APPLICANT: Silverman, Gregg J.
APPLICANT: Silverman, Gregg J.
ATILE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Chien, Wolfgang APPLICANT: Minamisawa, Susanne
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
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Publication No. US20040121942A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 16; Conservative
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CRGANISM: Homo sapiens
US-10-705-791-1
                                                                               ) ORGANISM: Homo sapiens
US-10-408-765A-478
        SEQ ID NO 478
LENGTH: 52
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US-10-705-791-2
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APPLICANT:
APPLICANT:
                                                         TYPE: PRT
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APPLICANT: Minamisawa, Susanne
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: Markus
APPLICANT: Markus
APPLICANT: Mang, Yibin
APPLICANT: Silverman, Yibin
APPLICANT: Silverman, OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REPERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: US/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR PILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
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TITLE OF INVENTION: COMPOUND SCREENING METHODS FILE REFREENCE: DOSS90.7013.US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATCHTIN VET: 2.0
SEQ ID NO 14
LENGIH: 52
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Publication No. US20040121942A1
GENERAL INFORMATION:
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SOFWARE: Patentin version 3.2
SEQ ID NO 5
LENGTH: 52
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US-10-705-791-5
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US-10-705-791-13
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                                                                APPLICANT: Ne, neue,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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US-09-954-571-3
i Gadence 3, Application US/09954571
i Publication No. US2002003167A1
i Publication No. US2002003167A1
i GREEAL INFORMATION:
    APPLICANT: Chien, Kenneth R
    APPLICANT: Chien, Kenneth R
    APPLICANT: Ross, John
    TITLE OF INVENTION:
    TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
    TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
    TITLE OF INVENTION UNDER: US/09/954,571
    CURRENT APPLICATION NUMBER: 60/231,821
    PRIOR PLILING DATE: 2001-09-11
    PRIOR FILING DATE: 2001-10-09
    NUMBER OF SEQ ID NOS: 5
    CONTINUER: PRICHING VERSION 3.2
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US-10-371-101-14
US-10-371-101-14
Sequence 14, Application US/10371101
Publication No. US20030149995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
            Minamisa...
He, Huaping
'''ma, Masahiko
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; ORGANISM: Canis familiaris
US-09-954-571-3
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LENGIH: 52
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APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: 06/106,718
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PC7/US99/25692
PRIOR FILING DATE: 1999-11-02
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 79
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| Publication No. US20020032167A1
| Publication No. US20020032167A1
| Publication No. US20020032167A1
| APPLICANT: Chien, Kenneth R
| APPLICANT: Chien, Kenneth R
| APPLICANT: Ross, John
| APPLICANT: Ross, John
| APPLICANT: Ikeda, Yasuhiro
| TITLE NETERBNCE: 6627-PA0123
| CURRENT FILING DATE: 2001-09-11
| PRIOR APPLICATION NUMBER: US/09/954,571
| PRIOR APPLICATION NUMBER: 06/231,821
| PRIOR PLING DATE: 2000-11-09
| NUMBER OF SEQ ID NOS: 5
| SOFTWARE: Patentin version 3.2
| LENGTH: 52
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100.0%; Pred. No. 1.1e-05;
tive 0; Mismatches 0; Indels
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US-09-954-571-1
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APPLICANT: Hoshijina, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
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Dillmann, Wolfgang
Minamisawa, Susanne
                         1 MEKVOYLTRSAIRRA 15
                                                                                  1 MEKVOYLTRSAIRRA 15
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; ORGANISM: Escherichia coli
US-10-705-791-18
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Best Local Similarity
Matches :15; Conserva
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ORGANISM: Artificial
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US-10-705-791-18
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TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: USABLE SISTEMATE SILVERMAIN ACTIVITY FOR THE TREATMENT
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION WUMBER: 60/106,718
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
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TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: 60/106,718
PRIOR PELING DATE: 1998-11-02
PRIOR PLING DATE: 1999-11-02
PRIOR FILING DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: PACHURA DATE: 
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94.7%; Score 71; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                         The Regents of the University of California Chien, Kenneth Dillmann, Wolfgang
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Hoshijima, Masahiko
Meyer, Markus
Scott, Christopher
Wang, Yibin
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Hoshijima, Masahiko
Meyer, Markus
Scott, Christopher
Wang, Yibin
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Publication No. US20040121942A1
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; ORGANISM: Homo sapiens
US-10-705-791-13
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; ORGANISM: Homo sapiens
US-10-705-791-12
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Best Local Similarity
.....hes 15; Conserva
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SEQ ID NO 12
                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                       APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: He Huaping
APPLICANT: He Huaping
APPLICANT: He Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Scott, Christopher
APPLICANT: Silverman, Gregg J.
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT:
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: 01/10/106,718
FRIOR PRILOR DATE: 1998-11-02
FRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 6
ILENGTH: 52
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US-10-424-599-218702
Sequence 238702, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21(35223)8
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                             Length 52;
                                                                                                                                                                                                           92.0%; Score 69; DB 16; Length 52
93.8%; Pred. No. 2.5e-05;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Regents of the University of California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10705791; Publication No. US20040121942A1; GENERAL INFORMATION:
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chien, Kenneth
Dillmann, Wolfgang
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Best Local Similarity 93.8%
Matches 15; Conservative
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                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-705-791-3
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US-10-705-791-6
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Best Local Similarity
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APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: Ho, Huaping
APPLICANT: Socut. Christopher
APPLICANT: Socut. Christopher
APPLICANT: Silverman, Gregg J.
TITLE OF INVEXTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVEXTION: OF CARDIAC DISEASE
TITLE OF INVEXTION: OF CARDIAC DISEASE
TITLE OF INVEXTION: OF CARDIAC DISEASE
TITLE OF INVEXTION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR PELICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION NUMBER: PCT/US99/106,718
PRIOR APPLICATION NUMBER: PCT/US99/106,718
PRIOR APPLICATION NUMBER: PCT/US99/25692
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Minamisawa, Susanne
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Sidiam, Masahiko
APPLICANT: Mayer, Markus
APPLICANT: Mayer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAWBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAWBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT FILING DATE: 2003-11-10
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
                               0; Gaps
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Pred. No. 1.7e-05;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                           Sequence 4, Application US/10705791
Publication No. 192040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Dillnann, Wolfgang APPLICANT: Minamisawa, Susanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Dillmann, Wolfgang APPLICANT: Minamisawa, Susanne
                         ..
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 93.83
Matches 15; Conservative
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US-10-705-791-4
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US-10-705-791-3
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Sequence 46161, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: APABLICANT: Cao, Yongwei

APPLICANT: Tabaska, Jack E

APPLICANT: Geo, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REPRENCE: 38 = 21 (531313) B

CURRENT APPLICANTON: Plants and USes Thereof for Plant Improvement

FILE REPRENCE: 38 = 21 (531313) B

CURRENT APPLICANTON NUMBER: US/10/425,114

CURRENT APPLICANTON NUMBER: US/10/425,114

CURRENT APPLICANTON NUMBER: US/10/425,114

SEQ ID NO 46161

LENGTH: 68
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                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.2%; Pred. No. 3.5;
Matches 6; Conservative 5; Mismatches 2; Indels
                                                                                                           FEATURE:

, OTHER INFORMATION: Clone ID: PAT_MRT3847_57573C.1.pep

US-10-424-599-238702
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; OTHER INFORMATION: Clone ID: 701164165_FLI.pep
US-10-425-114-46161
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Sequence 10177, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: INEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: HARINA, HARUO
APPLICANT: HARINA, HAROSHI
APPLICANT: HARINA, HAROSHI
APPLICANT: SATAKI, YOSHIVUKI
APPLICANT: SATKI, YOSHIVUKI
APPLICANT: SATKI, YOSHIVUKI
APPLICANT: SATKI, YOSHIVUKI
APPLICANT: SATKI, YOSHIVUKI
APPLICANT: BATORI, MASAHIRA
TITLE OF INVENTON: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
FRIOR APPLICATION NUMBER: UP 2001-272697
FRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109
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25 LEKIEYITRERIK 37
                                                                                                                                                                                                                                                                                                                                 1 MEKVQYLTRSAIR 13
                                                     TYPE: PRT
ORGANISM: Glycine max
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SEQ ID NO 238702
LENGTH: 44
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; LENGTH: 116
; CROBANES PAT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-1017

Query Match
Best Local Similarity 46.7%; Score 41; DB 14; Length 116;
Best Local Similarity 46.7%; Pred. No. 10;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEKVQYLIRSAIRRA 15

Qy 1 NEKIEVYRGDVRRA 95

Search completed: October 1, 2004, 12:48:43
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October 1, 2004, 12:05:26 ; Search time 15.6 Seconds (without alignments) 98.658 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 100 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *
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Perfect score:
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                                                                                                                                                                                                                        Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | ð              |        |            | SUMMARIES |                    |
|---------------|-------|----------------|--------|------------|-----------|--------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB         | ΙD        | Description        |
|               | 75    | 100.0          | 52     | <u>.</u> H | A40424    | phospholamban - hu |
| 2             | 75    | 100.0          | 52     | ч          | 537638    | phospholamban - ra |
| m             | 75    | 100.0          | 52     | Н          | A49057    | phospholamban - mo |
| 4             | 75    | 100.0          | 52     |            | B40424    | 1                  |
| S             | 72    | 96.0           | 52     | Н          | A29002    | 1                  |
| 9             | 72    | 96.0           | 52     |            | S05540    | phospholamban - pi |
| 7             | 71    | 94.7           | 52     |            | A39535    | •                  |
| 80            | 41    | 54.7           | 116    |            | T34780    | ribosomal protein  |
| σ             | 41    | 54.7           | 451    |            | F75083    | $\sim$             |
| 10            | 40    | 53.3           | 121    |            | B70187    |                    |
| 11            | 40    | 53.3           | 1108   |            | E71104    | probable cell divi |
| 12            | 8     | 52.0           | 481    |            | B75167    |                    |
| 13            | 38    | 50.7           | 119    |            | D69155    |                    |
| 14            | 37    | 49.3           | 283    |            | H69179    | $\rho$             |
| 15            | 37    | •              | 296    |            | F70879    | hypothetical prote |
| 16            |       | 49.3           | 308    |            | AC1867    |                    |
| 17            |       | 4              | 2712   |            | TOS113    |                    |
| 18            | 36    | 48.0           | 236    |            | D69048    | d hyp              |
| 19            | 36    | 48.0           | 294    |            | T00104    | probable dTDP-4-de |
| 20            |       | 48.0           | 335    |            | A24785    | hypothetical prote |
| 21            | 36    | 48.0           | 409    | N          | F83493    |                    |
| 22            |       | 48.0           | 410    |            | T12833    | hypothetical prote |
| 23            |       | 48.0           | 417    |            | H83370    | hydrogen cyanide s |
| 24            |       | 48.0           | 434    |            | T04263    | phosphoprotein pho |
| 25            | 36    | ٠              | 462    |            | AH1053    | probable exported  |
| 26            |       | 48.0           | 486    |            | I55449    | -                  |
| 27            | 36    |                | 549    |            | A90253    | hetical p          |
| 28            | 36    | 48.0           | 622    |            | JC5425    | H                  |
| 53            | 36    | 48.0           | 736    |            | 169       | dishevelled homolo |

| hexokinase (EC 2.7 transcription-repa hypothetical prote hypothetical prote aliphatic amidase transcription regulyothetical prote cysteine synthase porphobilinogen sy conserved hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote | San San San San San San San San San San               | NADH2 dehydrogenas ribosomal probable ribosomal protein probable ribosomal protein hypothetical protein hypothetical protein probable outer mem hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | S C C C C C C C C C C C C C C C C C C C    |
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| 0448000000004040400                                                                                                                                                                                                                                                                                                                                         | 1777770000NHNH0H0N                                    | 11111111111111111111111111111111111111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | - COOOD                                    |
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phospholamban - mouse
C;Species: Mus musculus (house mouse)
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
S;Ganim, J.R.; Luo, W.; Ponniah, S.; Grupp, I.; Kim, H.W.; Ferguson, D.G.; Kadambi, V.; R;Garim, J.R.; Luo, M.; Ponniah, S.; Grupp, I.; Kim, H.W.; Ferguson, D.G.; Kadambi, V.; R;Garence: Musculus (house)
A;Reference number: A49057; MUD:93008802; PMID:1394867
A;Residues: 1-52 GAN>
A;Residues: 1-52 GAN>
A;Residues: 1-52 GAN>
A;Residues: 1-52 GAN>
A;Residues: 1-52 GAN>
A;Residues: 1-52 GAN>
A;Ross-references: GB:846792; NID:9257745; PIDN:AAB23706.1; PID:9257746
A;Ross-references: GB:846792; NID:9257745; PIDN:AAB23706.1; PID:9257746
A;Residues: 1-52 GAN>
A;Cross-references: GB:846792; NID:9257745; PIDN:AABC3706.1; PID:9257746
A;Residues: 1-52 GAN>
A;Cross-references: GB:846792; NID:9257745; PIDN:AABC3706.1; PID:9257746
A;Residues: 1-52 GAN>
A;Cross-references: GB:846792; NID:9257745; PIDN:AABC3706; NICEIP:117001)
C;Comment: Phospholamban is the major phospholated and the rate of muscle sarcoplasm
C;Keywords: acetylated anno end; ATPase inhibitor; muscle; pentamer; phosphorein; transmembrane #status predicted
F;17/Binding site: phosphate (Firl) (covalent) (by calmodulin-dependent kinase) #status predicted
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase)
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Classian Orders and Comestic rabbit)

Classian 192 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999

Clacession: B40424; S00249

Classion: B40424; S00249

Classion: Chem. 266, 11669-11675, 1991

A; Tailo: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignates compared number: A40424; MUID:91268012; PMID:1828805

A; Reference number: DNA, A6024; MUID:91268012; PMID:1828805

A; Residues: 1-52 <FUJ
                                                                                 A; Molecule type: mRNA
A; Residues: 1-52 c4MA2>
A; Residues: 1-52 c4MA2>
A; Residues: 1-52 c4MA2>
A; Residues: 1-52 c4MA2>
A; Cross-references: GB:S95849; NID:9247934
C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplash Pase; after phosphorylation, the calcium pump is activated and the rate of muscle relaxat; C; Superfamily: phospholamban caddiac mino end; ATPase inhibitor; cardiac muscle; heart; pentamer; phos; F; Nacy activated amino end; ATPAS and (Met) #status predicted
F; Modified site: acctylated amino end (Met) #status predicted
F; Modified site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predicter
F; 17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase)
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A;Accession: 151840
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Cipaces (D-Mar-1994 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
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Richard (D-Mar-1994 #sequence revision 0 farger markers of differentiated and proliferating vascular smooth markers of great markers of differentiated and proliferating vascular smooth markers (D-Mar)
A; Reference number: S37637; MUID:93284726; PMID:8508530
A; Residues: 1-52 commun. 188, 927-933, 1992
A; Title: Identification of a highly conserved region at the 5' flank of the phospholamba A; Reference number: 152270; MUID:93075183; PMID:1445334
A; Accession: 15220
A; Title: Lidentification of a highly conserved region at the 5' flank of the phospholamba A; Accession: 152270
A; Coss-references: GB:L03382; NID:9206134; PIDN:AAA41849.1; PID:g206136
A; Residues: 1-52 cuOH>
A; Residues: 1-52 cuOH>
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A; Residu
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K;Fulii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
J. Biol. Chem. 266, 11669-11675, 1991
A;Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assi
A;Reference number: A40424; MUID:91268032; PMID:1828805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-52 <FUJ>
A; Residues: 1-52 <FUJ>
A; Cross-references: GBN MG3603; NID:g189942; PIDN: AAA60083.1; PID:g189943
C; Comment: Phospholamban is expressed in Cardiac muscle, slow twitch skeletal muscle, an
C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
c; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C; Comment: Helical transmembrane domains of five chains are thought to aggregate in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: GDB:PLN; PLB
A;Cross-references: GDB:128300; OMIM:172405
A;Mcross-references: GDB:128300; OMIM:172405
A;Mcross-references: GDB:128300; OMIM:172405
A;Map position: 6q22.1-6q2.1
C;Superfamily: phospholambar
C;Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr F;31-52/Domain: transmembrane #status predicted TF;Modified site: acetylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status F
                                                                                                                                                                                                                                                                                          Species: Homo sapiens (man)
Date: 28-Reb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
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A;Stcus: preliminary; translated from GB/EMBL/DDBJ
A;Rocule type: mRNA
A;Residues: 1-52 <HWAl>
A;Residues: 1-52 <HWAl>
A;Cross-references: GB:S95853; NID:g247932; PIDN:AAB21903.1; PID:g247933
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ALIGNMENTS
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Best Local Similarity 100.0
Matches 16, Conservative
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A,Accession: 146227
A,Status: translated from GB/EMBL/DDBJ
A,Accession: 145227
A,Gatutes: translated from GB/EMBL/DDBJ
A,Status: translated from RNA
A,Residues: 1-52 < dVZ
A,Residues: 1-52 < dVZ
A,Cross-references: GB:M5393; NID:g164045; PIDN:AAC41618.1; PID:g164046
C,Comment: Phospholamban is the major phosphorylated protein in cardiac muscle, and C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation ir C;Reywords: accepylated anano end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane #status predicted <pre>cPMA-ST-S-Domain: transmembrane #status predicted cPMA-ST-S-Domain: transmembrane #status (Met) #status experimental
F;I,Madified site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status experime F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status experimental
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CySpecies: Sus scrofa domestica (domestic pig)
CyDate: Sus scrofa domestica (domestic pig)
CyAccession: 805540
Ryerboomen, H.; Wuytack, F.; Eggermont, J.A.; de Jaegere, S.; Missiaen, L.; Raeymaekers,
Biochem, J. 262, 353-356, 1989
A;Title: CDNA cloning and sequencing of phospholamban from pig stomach smooth muscle.
A;Reference number: 805540; MUID:90056437; PMID:2530978
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A. Molecule type: mRNA
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A. Molecule type: mRNA
A. Molecule type: mRNA
A. Cross-references: BMBL:X15075; NID:g2055; PIDN:CAA33171.1; PID:g2056
A. Cross-references: BMBL:X15075; NID:g2055; PIDN:CAA33171.1; PID:g2056
C. Comment: Phospholamban is expressed in cardiac muscle, slow twitch selected muscle sarcoplast
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation in C. Superfamily: phospholamban
C. K. Superfamily: phospholamban
C. K. Superfamily: phosphorylated and the status predicted <TMM>
F;31-52/Domain: transmembrane #status predicted <TMM>
F;31-52/Domain: transmembrane #status predicted <TMM>
F;31-52/Domain: transmembrane #status predicted (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by Calmodulin-dependent kinase) #status predicte
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase)
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 06-Mar-1992 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
C;Dates: 106-Mar-1992 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
R;Toyofuku, T: Zak, R.
J. Biol. Chem. 266, 5375-5383, 1991
A;Title: Characterization of cNNA and genomic sequences encoding a chicken phospholamban.
A;Reference number: A39535; MUID:91170195; PMID:1825996
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A,Residues: 1-17,'L',19-52 <TOY>
A)cross-references: GB:M59039; NID:g212575; PIDN:AAA62738.1; PID:g212576
A)Note: the authors translated the codon CTT for residue 18 as Ile
A,Accession: B39535
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Matches 15; Conservative
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F;31-52/Domain: transmembrane #status predicted <TWM>
F;1/Modified site: acetylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
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C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Date: 23-Aug-1887 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Date: 23-Aug-1887 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Date: 23-Aug-1887 #sequence 18-Jun-1999
R;Fujii, J; Juno, A.; Xitano, X.; Tanaka, S.; Kadoma, M.; Tada, M.
J. Clin. Invest. 79, 301-304, 1987
Januari Complete complementary DNA-derived amino acid sequence of canine cardiac phosph
A;Reference number: A29002; MUID:87083954; PMID:3793929
                                                                                                                                                                                                                                                                                A Status: not compared with conceptual translation
A, Molecule type: mRNA
A, Molecule: 1-52 < FUZA
A, Conseries: 1-52 < FUZA
C, Comment: Phospholamban is expressed in Cardiac muscle, slow twitch skeletal muscle, an C; Comment: Phospholamban is expressed in Cardiac muscle, slow twitch skeletal muscle, an C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplase; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is
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R;Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
Nucleic Acids Res. 15, 6738, 1987
A;Itle: The CDNA sequence of the major phospholamban mRNA in canine cardiac ventricular A;Reference number: A26805; MUID:87316936; PMID:3628007
A;Accession: A26805
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A, Rosidues: 1-52 <UVE>
A, Cross-references: GB: Y00399, NID: 9911, PIDN: CAA68461.1; PID: 9912
A, Cross-references: GB: Y00399, NID: 9911, Theibert, J.L.; Wegener, A.D.; Jones, L.R.
J. Biol. Chem. 261, 1333-13341, 1986
A, Title: Sequence analysis of phospholamban. Identification of phosphorylation sites and A, Reference number: A25307, MUID: 87008549; PMID: 3759968
A, Contents: partial sequence and phosphorylation sites
A, Accession: A25307
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A,Residues: 1.35,'X',37-40,'X',42-45 <FU2>
R;Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
Nucleic Acids Symp. Ser. 17, 121-124, 1986
A;Title: Characterization of recombinant cDNA clones for canine cardiac phospholamban.
A;Reference number: 146227; MUID:87174860; PMID:3562256
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A Release Louis Louis Landa, M.; Toda, H.; Sakiyama, F.
R/Fujii, J.; Kadoma, M.; Tada, M.; Toda, H.; Sakiyama, F.
Biochem. Biophys. Res. Commun. 138, 1044-1050, 1986
A/Title: Characterization of structural unit of phospholamban by amino acid sequencing A/Reference number: A24818; MUID: 86323152; PMID: 3753485
A/Contents: partial sequence and acetylation site
                                                            FEBS Lett. 227, 51-55, 1988
A;Title: Rabbit cardiac and slow-twitch muscle express the same phospholamban gene. A;Reference number: S00249; MUID:88112222; PMID:2962883
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Pred. No. 5.4e-07;
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                  R; Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H
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Best Local Similarity 100.0
Matches 16; Conservative
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A, Residues: 1-52 < UYE>
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A; Residues: 1-52 <FUJ>
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Figure 19 protein 119 (rppls) - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Accession: BOYD187
C;Accession: BOYD187
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C;Accession: BOYD187
C;Accession: BOYD187
C; Farland, S; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, R.; White, Son, D; Peterson, J.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Attle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; FMID:9403685
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Status: DNA
A;Residues: 1-121 <a href="https://doi.org/10.100/">KMID:92688622</a>; PIDN:AACG7044.1; PID:92688622
A;Coss-references: GB:AE001170; GB:AE000783; NID:92688623; PIDN:AACG7044.1; PID:92688625
A;Experimental source: strain B31
C;Superfamily: Escherichia coli ribosomal protein L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable cell division control protein - Pyrococcus horikoshii probable cell division control protein - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Spacession: E71104

R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine R; Cohikuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA, Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic and A;Reference number: A71000, MUID:98344137; PMID:9679194

A;Accession: E71104

A;Accession: E
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A;Coss-references: GB:AP000003; NID:g3236130; PIDN:BAA29695.1; PID:d1030638; PID:g325703
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
                                              A,Molecule type: DNA
A,Residues: 1-451 «KAW»
A/Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB49971.1; PID:g545848:
A;Experimental source: strain Orsay
C;Genetics:
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                                                                                                                                                                                                                                                                                                                         A;Gene: PAB1666
C;Superfamily: phosphomannomutase
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Best Local Similarity 53.33
Matches 8; Conservative
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Best Local Similarity 53.34
Matches 8; Conservative
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Best Local Similarity
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B70187
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A; Rolecule type: DNA
A; Residues: 1-52 <TO2>
A; Cross-references: GB:M59038
A; Cross-references: GB:M59038
A; More: the sequence of residues 33-52 and the corresponding nucleotide sequence are not R; Toyothku, T.; East, R. submitted to GenBank, April 1991
A; Reference number: A44531
A; Reference number: A44531
A; Residues: 1-52 <TO3>
A; Residues: 1-52 <TO3>
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A; Residues: 1-52 <TO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Cross-references: 48.M5938
A.Cross-references: 48.M5938
C.Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an C.Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas c.Comment: Phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is clearetics:
C.Genetics:
A.Note: only one gene was detected
A.Note: the single intron is upstream of the coding region
C.Superfamally: phospholamban
C.Superfamally: phospholamban
C.Styerfamally: phospholamban estatus predicted CTMM>
F.31-52/Domain: transmembrane #status predicted CTMM>
F.31-52/Domain: transmembrane (Ser) (covalent) (by caMP-dependent kinase) #status predict F:16/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predict F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
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C;Species: Pyrococcus abyssi
C;Species: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F75683
R;anonymous, Genoscope
Submitteed to the BMBL Data Library, July 1999
A;Pescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
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A, Experimental source: strain A3(2)
A, Genetics:
A, Genetics: CSEDB: SC2E1.12
C; Superfamily: Escherichia coli ribosomal protein L19
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C;Species: Streptomyces ccelicolor

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000

C;Accession: T34760

R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1998

A;Reference number: Z21557
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DM
A;Residues; 1-116 *MIR>
A;Residues; 1-116 *MIR>
A;Cross-references: EMBL:AL023797; PIDN:CAA19387.1;
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Best Local Similarity 46.7%
Matches 7; Conservative
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hypothetical protein alro484 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. pcC 7120
C;Species: Nostoc sp. pcC 7120
C;Accession: Ac1867
C;Accession: Ac1867
C;Accession: Ac1867
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res: 8, 265-213, 2001
C;Accession: Ac1867
C;Accession: Ac1867
A;Accession: Ac1867
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A;Accession: Ac1867
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:99295987; PMID:9634230
                                                                                                                                 A)Status: preliminary, nucleic acid sequence not shown, translation not shown A;Molecule type: DNA, **Residues: 1-283 **ATHA**
A)Kesidues: 1-283 **ATHA**
A)Cross-references: GB:Ab000842; GB:Ab000666; NID:g2621676; PiDN:AAB85107.1; PID:g262168
A)Experimental source: strain Delta H
                   A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15547.1; PID:e117388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Status: preliminary
A; Motecule type: DNA
A; Modecule type: DNA
A; Residues: 1-308 - KUIR>
A; Cross-references: GB:BA000019; PIDN:BAB72442.1; PID:g17129829; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: alr0484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Date: 17-Jul-1998 #Bequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
49.3%; Score 37; DB 2; Length 283;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB Pred. No. 42; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                             A,Gene: MTH601
C,Superfamily: hypothetical protein AF1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Experimental source: strain H37Rv
           179, 7135-7155, 1997
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Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 YLTREAFKRAA 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-296 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: Rv2751
           Bacteriol.
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R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Rismith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Olu, D.; Spadafora, R.; Vicalie, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Molecule type: DNA
A; Residues: 1-119 < MTH>
A; Residues: 1-119 < MTH>
A; Residues: 1-119 < MTH>
A; Cross-references: GB:AE000827; GB:AE000666; NID:92621499; PIDN:AAB84931.1; PID:9262149
                                                                                                                                                                                                                                                                                                            C.Accession: B75167
R.anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A.Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru A.Reference number: A75001
A.Accession: B75167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Status: preliminary
A Molecule type: DNA
A Residues: 1-481 «KAW»
A Cross-references: GB: AJ248284, GB: AL096836, NID: 95457730, PIDN: CAB49417.1, PID: 9545792
A Experimental source: strain Orsay
A Genetics:
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A,Experimental source: strain Delta H
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C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Accession: H69179
R, Smith, D.R.; Douceter-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oliv, D.; Spadafora, R.; Wicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein MTH425 - Methanobacterium thermoautotrophicum (strain Delta H) C;Species: Methanobacterium thermoautotrophicum (C;Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: WTH425
A;Start codon: TTG
C;Superfamily: Methanobacterium thermoautotrophicum hypothetical protein WTH425
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                                                                                                                                                                                                                                               Species: Pyrococcus abyssi
Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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                                                                                                                                                                                                             hypothetical protein PAB0334 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.7%; Score 38; DB 2; Length 119; ilarity 37.5%; Pred. No. 11; Conservative 6; Mismatches 4; Indels
                                  668 MEVKDYLTREEVRKA 682
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Matches 6; Conserv
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C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession: T00104
A;Title: X; Toshida, Y.; Yamashita, Y.; Koga, T.
Biochim. Biophys. Acta 1442, 409-414, 1998
A;Title: A; gene Cluster for 6-deoxy-L-calan synthesis in Actinobacillus actinomycetemcomi A;Title: A;gene Cluster for 6-deoxy-L-calan synthesis in Actinobacillus actinomycetemcomi A;Accession: T00104
A;Accession: T00104
A;Accession: translated from GB/EMBL/DbBJ
A;Aclecule type: DNA
A;Residues: 1-294 <NAK>
A;Residues: 1-294 <NAK>
A;Residues: 1-294 <NAK>
A;Accession: T00104
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A;Residues: 1-409 <STO>
A;Cross-references: GB:AE004551; GB:AE004091; NID:g9947135; PIDN:AAG04601.1; GSPDB:GN001:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apporbatical protein 335 - slime mold (Dictyostelium discoideum) transposon DIRS-1 ("Species: Dictyostelium discoideum ("Species: Dictyostelium discoideum ("Species: Dictyostelium discoideum ("Species: Dictyostelium discoideum ("Species: Dictyostelium Dictyostelium DIRS-1987 #sequence ("Species: Dictyostelium DIRS-1985 "A") 1985 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1986 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 1886 "A") 
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
B;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, K.; Lim, Jourge 406, 959-964, 2000
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A,Accession: FB3493
A,Status: preliminary
Date: 22-Jan-1999 #Bequence_revision 22-Jan-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 2; Length 409;
Pred. No. 91;
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C.Genetics:
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Matches 7, Conservative
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S. Smith, D. B., Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. B. Bacteriol. 179, 7135-7155, 1997

A. Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A. Reference number: A69000; MUD:98037514; PMID:9371463

A. Accession: D69048

A. Status: preliminary; nucleic acid sequence not shown; translation not shown
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N;Alternate names: dTDP-4-keto-L-rhamnose reductase
C;Species: Actinobacillus actinomycetemcomitans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-236 <MTH>
A;Residues: 1-236 <MTH>
A;Cross-references: GB:AE000899; GB:AE000666; NID:g2622468; PIDN:AAB85841.1; PID:g262247
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F28M20.240 - Arabidopsis thaliana
Cyspecies: Arabidopsis thaliana (mouse-ear cress)
Cyspecies: Arabidopsis thaliana (mouse-ear cress)
Cyspecies: Arabidopsis thaliana (mouse-ear cress)
Cyspecies: 13-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
Cyaccession: T05113
RyBevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, November 1998
A,Reference number: 21539
A,Reference number: 21539
A,Rocession: T05113
A,Rocession: T05113
A,Rocession: T05112
A,Cross-references: BMBL:AL031004
A,Experimental source: cultivar Columbia; BAC clone F28M20
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A;Map position: 4
A;Introns: 17/3; 240/1; 1950/1; 2118/3; 2381/1; 2599/3; 2645/1; 2679/2
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49.3%; Score 37; DB 2; Length 2712;
Best Local Similarity 63.6%; Pred. No. 4.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels
                                                                    Query Match

49.3%; Score 37; DB 2; Length 308;
Best Local Similarity 53.3%; Pred. No. 44;
Matches 8; Conservative 3; Mismatches 4; Indels
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Best Local Similarity 46.,..
Acc 7; Conservative
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A; Experimental source: strain PAO1
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A; Residues: 1-104,'V',
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                                       C,Genetics:
A,Gene: hcnC; PA2195
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B.Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Britich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Albuthors: Soulger, D.; Fritz, C.; Fujita, M.D.; Frington, J.; Fabret, C.; Ferrari, E. A.Authors: P.; Koningsteal, B.; Hilbert, H.; Holsappel, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mulcell, M.; Kieger, M.; Rivogh, S.; Kumano, M.; Kurita, K.; Lagidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteelle A; Authors: Schletch, S.; Schreeter, B.; Scotche, P.; Schiguchi, J.; Scekowska, A.; Scaro, T.; Winner, S.; Migh, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A; Authors: Yoshikawa, H.; Pamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.; Miller, The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                              C;Species: Bacillus subtilis phage SPBC2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C;Accession: T12833; E69915
B;Lazarevic, V; Duesterhosft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D. submitted to the EMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 propha A;Accession: T12833
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C;Jate: 15-89-2000 #sequence_revision 15-8ep-2000 #text_change 31-Dec-2000
C;Accession: H83370
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
1. Lory, S.; Olson, M.V.
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A;Molecule type: DNA
A;Residuss: 1-417 <STO>
A;Cross-references: GB:AE004646; GB:AE004091; NID:g9948213; PIDN:AAG05583.1; GSPDB:GN001
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A,Reference number: A82950; MUID:20437337; PMID:10984043
A,Accession: H83370
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58.3%; Pred. No. 92;
ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                               hypothetical protein yonV - Bacillus subtilis phage SPBc2
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A;Molecule type: DNA
A;Residues: 1-410 <LAZ>
       1; Mismatches
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7; Conservative
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                                                                                                                                 245 VOYLTRSGL 253
                                                                4 VQYLTRSAI 12
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probable exported protein STY4756 [imported] - Salmonella enterica subsp. enterica serovary probable exported protein STY4756 [imported] - Salmonella enterica subsp. enterica serovar Typhi
Gispecies: Salmonella enterica subsp. enterica serovar Typhi
Gispecies is also been called Salmonella typhi
Gispecies 19-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
Giscession: AH1053
Gispecies is revision 09-Nov-2001 #text_change 18-Nov-2002
Gispecies is revision Gispecies K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
Apathors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovia, R.; Reference number: AB0502; MUDD:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                      phosphoprotein phosphatase (EC 3.1.3.16) ABII - Arabidopsis thaliana
Nahlernate names: protein F20188.190
C)Alternate names: protein F20188.190
C)Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1599 #sequence_revision 30-Apr-1599 #text_change 08-Oct-1999
C;Accession: T04263; As588
C;Accession: T04263, As588
Submitted to the Protein Sequence Database, March 1999
A;Reference number: 215263
A;Reference number: 215263
A;Molegule: type: DNA
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A;Cross-references: EMBL:AL049483
A;Cross-references: Embl:AL049483
A;Experimental source: cultivar Columbia; BAC clone F20B18
R;Meyer, K.; Leube, M.P.; Grill, E.
Science 264, 1452-1455, 1994
A;Title: A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis tha A;Reference number: A54588; MUID:94255767; PMID:8197457
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A;Residues: 1-462 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06877.1; PID:g16505525; GSPDB:GN00176
C;Genetics:
                                                                                            Gaps
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                                Score 36; DB 2; Length 417;
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50.0%; Pred. No. ys.
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43.8%; Pred. No. 97;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: phosphoric monoester hydrolase
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                                                                                                                                                                2 EKVQYLTRSAIRRA 15
Query Match
Best Local Similarity 50.00
To Conservative
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Best Local Similarity 43.8%
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Map position: 4
A;Introns: 183/3; 280/3; 316/1
A;Note: F20B18.190
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A;Gene: STY4756

0; Gaps Query Match

48.0%; Score 36; DB 2; Length 462;
Best Local Similarity 53.8%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels

2 EKVQYLTRSAIRR 14 :|| ::|| ||| 294 DKVTWMTREASRR 306

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Search completed: October 1, 2004, 12:19:41 Job time : 15.6 secs

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RESULT 1
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GenCore version 5.1.6
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Maximum Match 100%
Listing first 100 summaries
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SYA_THBAC
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APAH_ACTAC
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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|----------------------------------------|--------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|----------------------------------------------------|--------------------------------|---------------------------------|--------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|-------------------------------|---------------------------------|----------------------------------|--------------------------------|--------------------------------|--------------------------------|-------------------------------|------------------------|-------------------------------|-------------------------------|-------------------------------|-------------------------------|-------------------------------|-------------------------------|-------------------------------|-------------------------------|------------------------|-------------------------------|-------------------------------|-------------------------------|------------------------------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|--------------------------------------------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|--------------------------|----------------------------------|----------------------------------|-----------------------------------------|---------------------------------------|--------------------------------------------|--------------------------------------------|-------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                                        | 3.4                | 0 W<br>1. 4.                    | 3.4                             | 34                              | ω.<br>4 4                       | ى<br>4. د                       | J) (J)                                             | ) (r                           | ) (c)                           | , W                      | 3.4                             | , c.                            | ν<br>4.                         | , 4,                            | . 6.<br>4.                    | 4.                              | 3.4                              | 33                             | 33                             | e e                            | m c                           | <br>                   | 2 C                           | າຕ                            | 33                            | 33                            | e e                           | m<br>m<br>v                   | n w<br>w w                    | ່ຕ                            | 3 E                    | 33                            | e e                           | 13 C                          | 0 m                                                  | 1 E                             | 33                              | 33                              | e e                             | 13 th                                                              | ) e                             | 33                              | 33                              | E) C                            | າຕ                              | 33                              | 33                              | 33                              | e c                      | m c                              | <br>                             | 3 (2)                                   | 33                                    | 33                                         | e e                                        | en c                                      | n m                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |

ALIGNMENTS

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Raplachon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Moorley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Matcheman M., Madan A., Rodrigues S., Sanchez A.,
Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=9126032;
MEDLINE=9126032;
MEDLINE=9126032;
MEDLINE=9126032;
MESTRUCTURE of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6.";
J. Biol. Chem. 266;11669-11675(1991).
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Mortishire-Smith R.J., Pitzenberger S.M., Burke C.J., Middaugh C.R.,
Garsky V.M., Johnson R.G.;
                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=99222499; PubMed=10198197; McTiernan C.F., Frye C.S., Lemster B.H., Kinder E.A., McTiernan C.F., McTiernan C.F., McTiernan C.F., McTiernan A.M.; McGetree-Hughes M.L., Moravec C.S., Feldman A.M.; "The human phospholamban gene: structure and expression."; J. Mol. Cell. Cardiol. 31:679-692(1999).
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Salvatore C.A., Jacobson M.A.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB).
    52 AA.
    PRT;
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    STANDARD;
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PPLA HUMAN
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PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
PHOSPHORYLATION (BY CAMK) (BY
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Herzyk P., Hubbard R.E.;

"Using experimental information to produce a model of the transmembrane domain of the ion channel phospholamban.";

Blophys. J. 74:1203-1214 (1998).

-! PUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.
-! SUBGNIT: Homopentamer.
-! SUBGNIT: Homopentamer.
-! TISSUE SPECIFICITY: Heart.
-! TISSUE SPECIFICITY: Heart.
-! PTM: Phosphorylated in response to beta-adrenergic stimulation.
-! SIMILARITY: Belongs to the phospholamban family.
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Oryctolagus cuniculus (Rabbit).
Sukarycta: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090, 10116, 9986;
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MIM: 172405; -.
InterPro.; IPR005984; P lamban. 1.
Pfam: PF04272; Phospholamban; 1.
IIGRPAMs; TIGR01294; P lamban; 1.
Transmembrane; Phosphorylation; Acetylation; 3D-structure.
Transmembrane; Phosphorylation; CYTOPLASMIC (POTENTIAL).
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Cart-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB).
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PDB, 1ECH; 28-NOV-01.
PDB, 1PLN; 29-DEC-99.
PDB, 1PLN; 31-UTL-95.
PDB; 1PSL; 03-JUN-95.
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SEQUENCE FROM N.A.

MEDLINE=98170970; PubMed=9512019;

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                                                                                                                                                                                                                                                                                                                Pujii J., Lytton J., Tada M., Maclennan D.H.; "Rabbit cardiac and slow-twitch muscle express the same phospholamban
                                                                Fujii J., Zarain-Herzberg A., Willard H.F., Tada M., Maclennan D.H., Structure of the rabbit phospholamban gene, cloning of the human CDNA, and assignment of the gene to human chromosome 6."; J. Biol. Chem. 266:11669-11675(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johns D.C., Feldman A.M.; "Identification of a highly conserved region at the 5' flank of the phospholamban gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ganim J.R., Luo W., Ponniah S., Grupp I., Kim H.W., Ferguson D.G., Kadambi V., Neumann J.C., Doetschman T., Kranias E.G.; "Mouse phospholamban gene expression during development in vivo and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in vitro.";
Circ. Res. 71:1021-1030(1992).
Circ. Res. 71:1021-1030(1992).
-!- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum. activity of the membrane.
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-!- TISSUB SPECIFICITY: Heart.
-!- FTM: Phosphorylated in response to beta-adrenergic stimulation.
-!- SIMILARITY: Belongs to the phospholamban family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shanahan C.M., Weissberg P.L., Metcalfe J.C.;
"Isolation of gene markers of differentiated and proliferating
Vascular smooth muscle cells";
Circ. Res. 73:1193-204(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=Rat; TISSUE-Aortic smooth muscle;
MEDLINE=92206263; PubMed=1725098;
Hwang K.S., Nadal-Ginard B.;
"Cloning phospholamban cDNA from rat aortic smooth muscle.";
Adv. Exp. Med. Biol. 304:387-395(1991).
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EMBL; M63600; -; NOT ANNOTATED_CDS.
EMBL; M63601; AAA31445.1; -.
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MEDLINE=88112222; PubMed=2962883;
                                        MEDLINE=91268032; PubMed=1828805;
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B40424.
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SPECIES=Rabbit;
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S37638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-45.

SEQUENCE OF 1-45.

MEDILINE=86323152; PubMed=3753485;
Fuji J., Kadoma M., Tada M., Toda H., Sakiyama F.;
Fuji J., Kadoma M. Tada M., Toda H., Sakiyama F.;
Fuji J., Radoma M. Tada M., Toda H., Sakiyama F.;
Fuji J., Radoma M. Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Toda M., Toda H., Sakiyama P.;
Fuji J., Radoma M., Tada M., Tada M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M., Toda M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris', "...."
Canis familiaris', Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI TaxID=9823, 9615;
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HSSP, P26678; 1r...

MGD, MGI-97622; Pln.

R InterPro; 1PR005984; P lamban.

DR Pfam; PF04272; Phospholamban; 1.

DR Transmembrane; Phosphorylation; Acetylation.

Transmembrane; Phosphorylation; Acetylation.

Transmembrane; Propertion; Acetylation.

Transmembrane; Propertion; Acetylation.

Transmembrane; Propertion; Propertion.

CYTOPLASMIC (POTENTIAL).

POTENTIAL).

ACETYLATION (BY SIMILARITY).

ACETYLATION (BY EKA) (BY SIMILARITY).

Transmembrane; Propertion (BY SIMILARITY).
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SECLES=C.familiaris,
MEDLINE=87000549; PubMed=3759968;
Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75; DB 1; Length 52;
Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07), Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ...
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Nucleic Acids Res. 15:6738-6738(1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=C.familiaris;
MEDLINE=87083954; PubMed=3793929;
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SPECIES=C.familiaris;
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SPECIES-Pig; TISSUE-Smooth muscle;
MEDILNE=90056437; PubMed=2530378;
MEDICOMEN H., Wuytack F., Eggermont J.A., de Jaegere S.,
Missiaen L., Raeymaekers L., Casteels R.;
"cDNA cloning and sequencing of phospholamban from pig stomach smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                    Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; "Phospholamban phosphorylation in intact ventricles. Phosphorylation of serine 16 and threonine 17 in response to beta-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1. FUNCTION: Phosphologian has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum. SUBUNIT: Homopentamer: -1. SUBCHLULAR LOCATION: Membrane. -1. TISSUE SPECIFICITY: Heart. -1. TISSUE SPECIFICITY: Heart. -1. PTM: Phosphorylated in response to beta-adrenergic stimulation. -1. PTM: Bolongs to the phospholamban family.
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ACETYLATION (BY PKA).
PHOSPHORYLATION (BY CAMKI).
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01-AUG-1992 (Rel. 23, Last sequence update) -
28-FEB-2003 (Rel. 41, Last annotation update)
Cardiac phospholamban (PLB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 AA.
                                                                                                                  stimulation.";
J. Biol. Chem. 264:11468-11474(1989).
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MEDLINE=89291905; PubMed=2544595;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J. 262:353-356(1989)
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EMBL; Y00399; CAA68461.1; -.
EMBL; M35393; AAC41618.1; -.
EMBL; X15075; CAA33171.1; -.
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PIR, S05540; S05540.
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P26677;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way wordiside and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
PHOSPHORYLATION (BY CAMK) (BY
                                                                                                                                                                                                                                                                                                                        -i-TISSUE SPECIFICITY: Heart.
-i- PIM: Phosphorylated in response to beta-adrenergic stimulation.
-i- SIMILARITY: Belongs to the phospholamban family.
SEQUENCE FROM N.A. PubMed=1825996;
MODILINE=91170195; PubMed=1825996;
MOYOFUKU T., Zak R.;
"Characterization of cDNA and genomic sequences encoding a chicken
                                                                                                                                                        7. Biol. Chem. 266:5375-5383(1991).
-!-FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.
-!- SUBUNIT: Homopentamer.
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MEDLINE=21477403; PubMed=11572948;
Omuta S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
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Streptomycineae, Streptomycetaceae, Streptomyces.
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Pred. No. 7.6e-07;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASP, P26679, 1PLP.

ASSP., P26679, 1PLP.

InterPro; P86679; Plamban.

Pfam; PF04272; Phospholamban; 1.

TIGRFAMS; TIGR01294; Plamban; 1.

Transmembrane; Phosphorylation, Acetylation.

Transmembrane; Phosphorylation, Acetylation.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F95F86C36A0C4D3B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q82JW4;
1S-MAR-2004 (Rel. 43, Created)
1S-MAR-2004 (Rel. 43, Last sequence update)
1S-MAR-2004 (Rel. 43, Last annotation update)
50S ribosomal protein L19.
RPLS OR SAV2640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STMTIARITMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; MS9037; -; NOT ANNOTATED_CDS.
EMBL; MS9038; AAA63167.1; -
PIR; A39535; A39535.
                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEKVOYITRSALRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 AA; 6091 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M59039; AAA62738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=33903;
                                                                                                                                   phospholamban.";
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SPECIES=S.lividans; STRAIN=TK21;

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                                                    MEDINERALOGONOUS, TUDECULIANCE A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.; Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.; Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.; Shinosalive analysis of the industrial microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:526-531(2003)

-!-FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-CRNA binding site (By similarity).

-!-SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINES-19964010, PubMed=12000953,
Benchey S. D., Chater K.F., Corden-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
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Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902, 1916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.7%; Score 41; DB 1; Length 116; 46.7%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP, MF 00402, -; 1.
InterPro; IPR001857; Ribosomal L19.
Pfam, PF01245; Ribosomal L19; 1.
PRINTS, PR00061; RIBOSOMALL19; 1.
PRODOM; PD002979; Ribosomal L19; 1.
PTGREAMS; TTGR01024; FDIS bact; 1.
PROSITE; PS01015; RIBOSOMĀLL19; 1.
RIBOSOMAI PYCTEIN; COMPLETE PYCTEOME.
SEQUENCE 116 AA; 13186 MW; 47081773B07F6EB6 CRC64;
                     STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-REB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L19.
RPLS OR SOSSES OR SC2B.12.
Streptomyces coelicolor, and
Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 116 .AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP005031; BAC70351.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
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                  Parro V., Mellado R.P.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRATS-ATC 53210 / B31;
MEDLINE-398065943; PubMed-9403685;
MEDLINE-398065943; PubMed-9403685;
Lathigra R., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey B.K., Gwinn M.,
Dougherty B., Tomb J.-F., Flaischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
-i- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.7%; Score 41; DB 1; Length 116; 46.7%; Pred. No. 1; 3; Indels cive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37D782C6763D0A90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Dast sequence update)
28-FEB-2003 (Rel. 41, Dast annotation update)
50S ribosomal protein L19.
                                                                                                                                                                                                                                                                                                                                                   EMEL, Z86111; CABG6800.1; -.
PIR: T14780; T34780...; -.
HAMPE MF 00402; -.; 1.
IMMERPIO, IPRO01857; Ribosomal L19.
PFAM; PF01845; Ribosomal L19; P. PRINTS; PRO0061; RIBOSOMALLI9.
PRODOM; PD0022979; Ribosomal L19; 1.
TIGRFAMS; TIGR01024; rplS_bact; 1.
Ribosomal protein; Complete profesor.
SEQUENCE 116 AA; 13142 MW; 37D7820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteome
                                                                                                                                                                                                                                                                                                                                      EMBL; AL939124; CAA19387.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEKVQYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *||:::||:
81 VEKIELVTRGDVRRA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 40...
Best Local Similarity 40...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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051642;
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EMBL; AE013104; AAM24679.1; -., HAME, ME 00402; -; 1. L. SOGMAL L19.
FLAM, PR 010402; -; 1. L. SOGMAL L19.
PEAN; PF01245; Ribosomal L19; 1.
PRINTS; PROMOGOLI, RIBOSOMALL19.
PRODOW; PD002979; Ribosomal L19, TIGREAMS; TIGRO1024; rp1S bact; 1.
PROSITE; PS010105; RIBOSOMAL.119; 1.
PROSITE; PS010105; RIBOSOMAL.119; 1.
PROSITE; PS010105; RIBOSOMAL.119; 1.
SEQUENCE 115 AA; 13395 MM; 9EBE9AIE
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                                                                                                                                                                          353 KVGYLARMLIRRA 365
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                                                                                                                         3 KVQYLTRSAIRRA 15
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les 6; Conservative
                                                                         9; Conservative
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                                                   Best Local Similarity
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                           Query Match
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PSD_CHLCV
                                                                         Matches
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR02318; LRNA-synt_2c.
PinterPro; IPR03193; LRNA-synt_Ala.
PEAM; PF01411; LRNA-synt_Zc; 1.
PRINTS; PR0980; TRNASNYTHALA.
TIGRPAMS; TIGR00344; alaS; 1.
PROSTEX, PS50860, AA TRNA_LIGASE II ALA; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase, ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to class-II aminoacyl.tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Alanyl-tena synthetase (EC 6.1.1.7) (Alanine--tena ligase) (Alars).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 407:508-513(2000)
--- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alanyl--ENA(Ala)
---- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.3%; Score 40; DB 1; Length 121; 53.3%; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                   14011 MW; A33F7B1E4DF24070 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 871 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                          HAMMS, MF_00402, -; 1.
InterPro; IPR001857; Ribosomal L19.
Pfam, PF01245; Ribosomal L19; I.
PRINTS; PR00661; RIBOSOMĀLL19.
ProDom; PD002979; Ribosomal L19; 1.
IGRRAMS; IGR01024; rD18_Dact; 1.
PROSITE; PS01015; RIBOSOWĀL L19; 1.
Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20479972; PubMed=11029001;
                                                                                                                       EMBL; AE001170; AAC67044.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL445065; CAC11978.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEKVOYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 IEKVEVLRRGKVRRA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                  B70187; B70187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALAS OR TA0849
                                                                                                                                                                       IIGR; BB0699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THEAC
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                          Gaps
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082113;
10-OCT-2003 (Rel: 42, Created)
10-OCT-2003 (Rel: 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65) [Contains:
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
52.0%; Score 39; DB 1; Length 871; 69.2%; Pred. No. 22; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoanaerobacter tengcongensis. Thermoanaerobacteriales; Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriacea; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length 115;
Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9EBE9A1B89D3122B CRC64;
                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN (BY SIMILARITY).
PHOSPHATIDYLSERINE DECARBOXYLASE ALFHA
CLAIN (BY SIMILARITY).
CLAZAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
CONVERTED TO A PYRUVOYL GROUP (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APATAC STANDARD; PRT; 275 AA.
052655;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (BC 3.6.1.41)
(Diadenosine tetraphosphatase) (Ap4A hydrolase) (Diadenosine 5',5'''-P1,P4-tetraphosphate pyrophosphohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                       "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
"Genome sequence of niche-specific genes in the evolution of the
Chlamydiaceae.",
Nucleic Acids Res. 31:2134-2147(2003).
-!- CATALYTIC ACTIVITY: Phosphatidyl-L.serine =
phosphatidylethanolamine + CO(2).
-!- COFACTOR: Pyruvoyl group (By similarity).
-!- COFACTOR: Pyruvoyl group (By similarity).
-!- SIMILARITY: Belongs to the phosphatidylserine decarboxylase
family. Subfamily 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP, MF 00663; -; 1.
InterPero, IPR003817; PS Dcarbxylase.
InterPero, IPR003221; PS Cacarb.
Pfam; PF02666; PS Dcarbxylase; 1.
IIGRFAMs; TIGR00163; PS decarb; 1.
Phospholipid blosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHATIDYLSERINE DECARBOXYLASE BETA
                                                                                                                                                                     MEDLINE-22569155; PubMed=12682364;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Faulsen I.T., Haidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A. Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M., Fraser C.M.;
                                                                            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila
NCBI_TaxID=83557;
  Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.7%; Score 38; DB 1; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6F8EB837D97EE4E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinobacillus actinomycetemcomitans (Haemophilus actinomycetemcomitans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 11;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE016997; AAP05666.1; -. 
TIGR; CCA00927; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 AA; 34223 MW;
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1 MKKLQYIDRSTNQRVT 16
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                   decarboxylase beta chain].
PSD OR CCA00927.
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                                                       Chlamydophila caviae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 7; Conserv
                                                                                                                                   SEQUENCE FROM N.A.
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Matches
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SEQUENCE FROM N.A.

SEQUENCE OF ATC 13902 / XV 101;

MEDLINE=2202145; PubMed=12024217;

Ad Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Ad Silva A.C.R., Maral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A Alves L.M.C., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A Alves L.M.C., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

A Faria J.B., Franco M.C., Greggio C.C., Gruber A.,

A Ratuyama A.M., Kishi L.T., Leite R.P., Lenos E.G.M., Lenos M.V.F.,

A Locali E.C., Medbado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

A Moreira L.M., Novo M.T.M., Okura V.K., Oliveira V.S.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira V.S.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Pereira H.A., Takita M.A., Tamira R.E., Teixeira E.C., Pezza R.I.D.,

A Trindade dos Santos M., Truffil D., Tsai S.M., White F.F.,
                                                                                                                                                                                                                                                                                                Saarela M., Fives-Taylor P.,
Subarited (JAN-1998) to the EMBL/GenBank/DDBJ databases.
Subarited (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Hydrolyzes diadenosine 5',5'''-Pl,P4-tetraphosphate to
yield ADP (By similarity)
-!- CATALWITC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate +
H(2)0 = 2 ADP.
-!- SIMILARITY: Belongs to the Ap4A hydrolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.3%; Score 37; DB 1; Length 275; 40.0%; Pred. No. 15; tive 6; Mismatches 3; Indels
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RNA polymerase sigma factor rpoD (Sigma-70)
RPOD OR XAC3788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00199; -; 1.
InterPro; IPR004617; ApaH.
InterPro; IPR004683; M-ppestrase.
InterPro; IPR006186; T_phtase_apaH.
Pfam; PF00149; Metallophos; I.
ProDom; PD000252; T_phtase_apaH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000252; T_phtase_apaH; 1.
TIGREAMs; TIGR00668; apaH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF043998; AAC00202.1; -.
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                NCBI_TaxID=714;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Setubal J.C., Kitajima J.P.;
"Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
Nature 417.459-463(2002).
-!-FUNCTION: The sigma factor is an initiation factor that promotes attachment of the RNA polymerase to specific initiation sites and then is released. This is the primary sigma-factor of this bacteria (By similarity).
-!-SIMILARITY: Belongs to the sigma-70 factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=97257506; PubMed=9103980; Salvini M., Bini E., Santucci A., Batistoni R.,; Mistone in the macronucleus of Blepharisma japonicum (Protozoa, Ciliophora, Heterorichida) "; FEMS Microbiol. Lett. 149:93-98(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03979; sigma70_r1_i; 1.
Pfam; PF00140; sigma70_r1_2; 1.
Pfam; PF04545; sigma70_r2; 1.
Pfam; PF04545; sigma70_r2; 1.
Pfam; PF04545; sigma70_r2; 1.
Pfam; PF04545; sigma70_r2; 1.
PRINTS; PR00046; SIGMA70PcT;
PROSITE; PS00715; SIGMA70_2; 1.
Transcription_regulation; Sigma factor; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 427 POLYMERASE CORE BINDING (POTENTIAL).
584 603 H-T-H MOTIF (BY SIMILARITY).
625 AA; 70084 MW; 6B7032460884C850 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blepharisma japónicum.
Enkaryota, Alvoclata, Cilióphora, Heterotrichea, Heterotrichida,
Blepharismides, Blepharisma.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histone H4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE012027; AAM38630.1; ...
InterPro; IPR009043; RNA_pol_sigma.
InterPro; IPR007631; sigma70_ner.
InterPro; IPR007127; sigma70_r1_1.
InterPro; IPR007427; sigma70_r1_1.
InterPro; IPR007624; sigma70_r2_1.
InterPro; IPR007624; sigma70_r2_1.
InterPro; IPR007634; sigma70_r3_1.
InterPro; IPR007634; sigma70_r3_1.
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Pfam; PF04546; Sigma70 ner; 1.
Pfam; PF03979; Sigma70 r1 1; 1
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es 8; Conserv
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P80738;
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          SO THE WAR WAS A SHARE THE SO THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF THE SOUTH OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salvini M., Bini E., Santucci A., Batistoni R.,
"H4 histone in the macronucleus of Blepharisma japonicum (Protozoa,
Ciliophora, Heterotrichida).",
FEMS Microbiol. Lett. 149:93-98(1997).
-!- FUNCTION: Histone H4, along with histone H3, plays a central role
in nucleosome formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
-:- SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146 bp of DNA.
-:- SIMILARITY: Belongs to the histone H4 family.
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146 bp of DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS00047; HISTONE H4; PARTIAL.
Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
                                                                                                                                           Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blepharisma japonicum.
Eukaryota; Alveolata; Ciliophora; Heterotrichea; Heterotrichida;
Blepharismidae; Blepharisma.
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                                                                                                                                                                                                                    Score 36; DB 1; Length 47;
Pred. No. 3.5;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 AA; 10722 MW; 64BBB2D65594607C CRC64;
                                                                                                                                                                 NON TER 47 47
SEQUENCE 47 AA; 4961 MW; D743BEA73B76BADA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .! SIMILARITY: Belongs to the histone H4 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-46, AND SEQUENCE OF 9-97 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            H41 BLEJA STANDARD; PRT; 97 AA. P80737; P90515; 01-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) Histone H4-1 (Fragment).
                                                                      InterPro; IPR001951; Histone_H4.
PRINTS; PR00623; HISTONEH4.
ProDom; P0001827; Histone_H4; 1.
PROSITE; PS00047; HISTONE_H4; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X97995, CAA66634.1; TAF.
INTERPROFILE, Hist TAF.
INTERPROFILES, Histone CORE D.
INTERPROFILES, HISTONE CORE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A5-3;
MEDLINE=97257506; PubMed=9103980;
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ProDom; PD001827; Histone H4; 1.
                                                                                                                                                                                                              Query Match
Best Local Similarity 53.8%;
Marches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [larity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                 2 EKVQYLTRSAIRR 14
                                                                                                                                                                                                                                                                                                                                 27 ENIOGITKPAIRR 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00417; H4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5961;
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                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
H41_BLEJA
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P2C1_ARATH
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                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 13:1572-1579(2003).
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacy1-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                          Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.,
                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomydetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.0%; Score 36; DB 1; Length 113;
40.0%; Pred. No. 9.1;
ive 5; Mismatches 4; Indels
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InterPro; IPR001857; Ribosomal L19.
Pfam; PF01245; Ribosomal L19; 1.

PRINTS; PR00061; RIBOSOMALL15.

ProDom; PD002979; Ribosomal L19; 1.

PIGREMAS; TIGR01024; PDIS Bact; 1.

PROSTIE; PS01015; RIBOSOMALL19; 1.

Ribosomal protein; Complete proteome.

SEQUENCE 113 AA; 13008 MW; 9BDIC9D25ADA453A CRC64;
                                                                                                                                                                                                                                                                   STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                                                15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
50S ribosomal protein 119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L19.
RPLS OR CGL2037.
                                                                                           PRT; 113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP005220; BAC18742.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEKVQYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium efficiens.
2 EKVQYLTRSAIRR 14
                          26 ENIÓGITKPAÍRR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                       RPLS OR CE1932
                                                                                           RL19 COREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RL19 CORGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RL19_CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                  RESULT 15
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                                                                                                                                                                                                       "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein is located at the 305-50S ribosomal subunit
interface and may play a role in the structure and function of the
aminoacy1-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Makaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacees; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. Columbia; TISSUE=Leaf;
MEDLINE=95007758; PubMed=7923358;
Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
"The A. thallana disease resistance gene RPS2 encodes a protein
containing a nucleotide-binding site and leucine-rich repeats.";
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P49557; Q43717; Q94C87; O1-FEB-1996 (Rel. 33, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-WAR-2004 (Rel. 41, Last sequence update) Protein phosphatase 2C ABI1 (EC 3.1.3.16) (PP2C) (Abscisic acidinsensitive 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meyer K., Leube M.P., Grill E.;
"A protein phospharese 2C involved in ABA signal transduction in
Arabidopsis thaliana.";
Science 264:1452-1455(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.0%; Score 36; DB 1; Length 113; 40.0%; Pred. No. 9.1; tive 5; Mismatches 4; Indels
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2692B361BAFBA229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 434 AA.
                                                                                               ŚEÓUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANT ASP-180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAR; MF 00402; -; 1.
InterPro; IPR01857; Ribosomal L19.
Pfam; PP01245; Ribosomal L19; 1.
PRINTS; PR01061; RiBOSOMALL19.
ProDom; PD002979; Ribosomal L19; 1.
TIGREAMS; TIGR01024; rplS bact; 1.
PROSITE; PS01015; RIBOSOMAL L19; 1.
Ribosomal protein; Complete protecome.
SEQUENCE 113 AA; 12875 MW; 2692B361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Landsberg erecta;
MEDLINE=94255767; PubMed=8197457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP005280; BAB99430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 IEKIEVIRRGDVRRA 94
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Best Local Similarity
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                                                                                                                                                                        Nakagawa S.;
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AM REDINES C. AM REDINE C., Wandle L. A., Rieger M.,

AM CALLEGAT L., McCALLED D., PRESZ ALDING M., BOULTY M., BANCICE I.,

AM NOCHINES C., MCCALLED D., PRESZ ALDING M., BOULTY M., BANCICE I.,

AM AND REDINES C., AM REDINES C., MARCHER F., MACHER P.,

AM AND REDINES C., RAMBORES C., CHARGE Y. C., VAN CHARLES C.,

AM MONOIPMAN P. KICH LANKHORE R., ROSE M., HAUL J., VAN CHARLES C.,

AM MONOIPMAN P., KICH LANKHORE R., ROSE M., HAUL J., VAN CHARLES C.,

AM MONOIPMAN P., KICH LANKHORE R., ROSE M., HAUL J., WANDLEY K.,

AM MONOIPMAN P., KICH LANKHORE R., ROSE M., HAUL J., WANDLEY K.,

AM MONOIPMAN P., KICH LANKHORE R., ROSE M., HAUL J., WANDLEY K.,

AM MONOIPMAN M., REATHANN D., CARAMER M., CALMBAY K.,

AND MONOIPMAN M., REATHANN B., REALD M., LEADERT T., H.,

AND ROSE A., BUNGKAR M., REATHANN B., REALD K.,

AND ROSE C., GHABAN M., MARTHANN B., REDINER T., H.,

AND ROSE C., GHABAN M., MARTHANN B., STOKEN S.,

AND ROSE C., GHABAN M., MARTHANN B., STOKEN S.,

AND ROSE C., GHABAN M., MARTHANN B., STOKEN S.,

AND ROSE C., GOON ONLY S., CIDEBAIL G., MUNGLER M., MARLING S.,

AND ROSE C., RAMBAN M., MARTHANN B., STOKEN S.,

AND ROSE C., RAMBAN S., SCHORLER P., HOBER S., FRANCE C.,

AND ROSE C., RAMBAN S., STATEMBRON S., TROON D., JOSES T.,

AND ROSE C., MANDLER R., MANDLE M., SCHORL K.,

AND ROSE C., MANDLER R., MANDLE M., SCHORL K.,

AND ROSE C., RAMBOR S., SCHORL K., MONDLE M., SCHORL K.,

AND ROSE C., MANDLE M., MARTHAN D., REDINES M., HADDERTAN D.,

AND ROSE C., MANDLE R., MARTHAN D., REDINES M., MARTHAN D., SCHORL K., MONDLE M., MARTHAN D., REARDEN S., GENER C., SCHORL M., MARTHAN D., SCHORL M., MARTHAN D., SCHORL M., MARTHAN D., SCHORL M., MARTHAN D., SCHORL M., MARTHAN D., SCHORL M., MARTHAN D., RESIDENCY M., MARTHAN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=29594850; PubMed=14593172;

Yamada K., Lim J., Dable J.M., Chen H., Shinn P., Palm C.J.,

Asuthin-Mewmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Ariyama K., Araxana H., Banno P., Bookser L., Brooks S.Y., Carninci P.,

Arakawa T., Banno P., Bookser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Rhan S., Koesema E., Ishida J., Jang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Natusaka M., Sakin M., Sakirai T.,

Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
                                                                                                            'Arabidopsis ABA response gene ABI1: features of a calcium-modulated
                     STRAIN-CV. COlumbia; TISSUE-Leaf;
MEDLINE-94255766; PubMed-7310981;
Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F.,
                                                                                                                                                     cience 264:1448-1452(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402:769-777(1999).
                                                                                                                               protein phosphatase.
SEQUENCE FROM N.A.
                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G -> D (WILTY PHENOTYPE AND ABA-INSENSTITUTE SEED GERMINATION AND GROWTH).
G -> R (IN REF. 5).
I -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
JO-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, alpha.isoform (PP2A, B subunit, B' alpha isoform) (PP2A, B subunit, B's alpha isoform) (PP2A, B subunit, Rs alpha isoform) (PP2A, B subunit, Rs alpha isoform) (PP2A, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Manganese, Multigene family; Calcium-binding. EF-HAND (POTENTIAL).
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                 phosphate.
-!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
-!- SIMILARITY: Belongs to the PP2C family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia: Eutheria, Primates, Catarrhini; Hominidae, Homo.
                                                                -i- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.0%; Score 36; DB 1; Length 434; 43.8%; Pred. No. 39; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 AA; 47505 MW; 4A4C54F04195F572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-VAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96064678; Pubmed=7592815;
McCright B., Virshup D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                       PIR, 104263; 104263.
HSSP; P35813; 1A60.
InterPro; 1PR002048; EF-hand.
InterPro; IPR001932; PP2C-like.
InterPro; IPR000222; PP2C.
                                                                                                                                                                                                                                                                                                                                        EMBL, X77116; CAA54383.1; -.
EMBL, AL049483; CAB39673.1; -.
EMBL, AL161564; CAB79463.1; -.
EMBL, AX035073; AAK59578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00018; EF HAND; 1.
PROSITE; PS01032; PPZC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 MSAAEYLSKLAIQRGS 411
                                                                                                                                                                                                                                                                                                     EMBL; X78886; CAA55484.1; -. EMBL; U12856; AAA50237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00481; PP2C; 1.
SMART; SM00331; PP2C SIG; 1.
SMART; SM00332; PP2CC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     llarity 43.8%;
Conservative
                                                 Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEKVOYLTRSAIRRAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Breast canc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Q15172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
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2A5A HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: PEZA consists of a common heterodimeric core enzyme, composed of a 36 kDa catalytic subunit (subunit C) and a 65 kDa constant regulatory subunit (PR65 or subunit A), that associates with a variety of regulatory subunits. Proteins that associate with the core dimer include three families of regulatory subunits B (the RZ/B/RR55/BS5, R3/a'/PR72/PR130/PRS9 and R5/B'/Bs6 families), the 48 kDa variable regulatory subunit, viral proteins, and cell signaling molecules.
-!- SUBCELLULAR LOCATION: Cyroplasmic.
-!- TISSUE SPECIFICITY: Widely expressed with the highest expression in heart and skeletal muscle.
                                                                                                                                                    TISSUE=Brain;
MEDINE=SG57417; PubMed=8694763;
MEDINE=SG57417; Van Hoof C., Andjelkovic N., Cron P., Stevens I.,
Merlevede W., Goris J., Hemmings B.A.;
Merlevede W., Goris J., Hemmings B.A.;
"The variable subunit associated with protein phosphatase 2A0 defines
                                                                                                                                                                                                                                                                                                                                                                                                                            MCDLINE-86555607, PubMed=8703017,
MCCright B., Rivers A.M., Audlin S., Virshup D.M.;
McCright B., Rivers A.M., Audlin S., Virshup D.M.;
McCright B., Rivers A.M., Audlin S., Virshup D.M.;
McCright B., Rivers A.M., Audlin S., Virshup D.M.;
McCright B., Rivers A.M., Audlin S., Virshup D.M.;
McCright B., Rivers A.M., Audlin S., Virshup D.M.;
McCright B., Rivers A.M., Audlin S., Virshup D.M.;
McCright B., Rivers A.M.;
vers A.M.;
McCright B., Rivers A.M.;
McCright B., Rivers A., Rivers A.M.;
McCright B., Rivers A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
"Identification of a new family of protein phosphatase 2A regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PIM: Phosphorylated on serine residues.
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H -> S (IN REF. 2; AA SEQUENCE).
R -> E (IN REF. 2; AA SEQUENCE).
D31407F7032A6D44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.0%; Score 36; DB 1; Length 486; Matches 7; Conservation
                                                                                                                         SEQUENCE OF 47-56; 129-132; 347-354; 448-462 AND 471-480.
                                                                                                                                                                                                                                                                                                                a novel multimember family of regulatory subunits.";
Biochem. J. 317:187-194(1996).
                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subunits.";
J. Biol. Chem. 270:26123-26128(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 451 R
486 AA; 56193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L42373; AAC37601.1; -. PIR; I55449; I55449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:9309; PPP2R5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 417.459-463 (2002).

-1- FUNCTION: The signa factor is an initiation factor that promotes attachment of the RNA polymerase to specific initiation sites and then is released. This is the primary signa-factor of this bacteria (By similarity).

-1- SIMILARITY: Belongs to the signa-70 factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00715; SIGMA70 1; 1.
PROSITE; PS00716; SIGMA70 2; 1.
Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 FOLYMERASE CORE BINDING (POTENTIAL).
502 H-T-H MOTIF (BY SIMILARITY).
69947 MW; 1F6CBCA093F7F1AF CRC64;
                                                                                                                                                          Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                   10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RNA polymerase sigma factor rpoD (Sigma-70).
  624 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMEL ADJUGATE AND AND AND SEGMENT AND AND SEGMENT INTERPROPERS SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENO TENDORATED SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIGMENT SIG
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                                               10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE012494; AAM42993.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426
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624 AA;
                                                                                                                                             RPOD OR XCC3736.
                                                                                                                                                                                                                                           NCBI_TaxID=340;
RPSD_XANCP
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DNA BIND
SEQUENCE
                    SBP4H2;
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2 EKVQYLTRSAIRRA 15 ||| || ::|:| 19 EKVDGFTRKSVRKA 32

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Query Match

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Query Match
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             ö
                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Magnesium-chelatase subunit chlD (Mg-protoporphyrin IX chelatase) (Mg-chelatase subunit D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
             Gaps
                                                                                                                                                                                                                                                                                                                             magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
                                                                                                                                                                                                                                                          Masuda T., Nakayama M., Ohta H., Takayama K.-I., "Cloning and sequencing of a chlD gene encoding a subunit of magnesium-chelatase from the cyanobacterium Synechococcus sp. PCC
                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a
                                                                                                                                                                                                                                                                                                                                                   -i- PATHWAY: Chlorophyll biosynthesis.
-i- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
-i- SIMILARITY: Contains I WWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
            ö
                                                                                                                                                                                                    Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.0%; Score 36; DB 1; Length 677; 58.3%; Pred. No. 63;
            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00382; AAA; 1.
SMART; SM00382; VWA; 1.
PROSITE; PS50234; VWFA; 1.
Photosynthesis; Chorophyll biosynthesis; ATP-binding.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLU/PRO-RICH.
; 7E2988E096DF5506 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                              677 AA
 50.0%; Pred, No. 57; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB003135, BAA20346.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR000523; Mg_chelatse_chii.
InterPro; IPR002035; VWF_A.
Pfam; PF01078; Mg_chelatase; 1.
Pfam; PF010092; vwa; 1.
                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                       (In) Plant Gene Register PGR97-091.
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                                                357 MEKANYLTLAEIKDIS 372
                                  1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 58.3%;
Conservative
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            Conservative
                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EKVQYLTRSAIR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 36
677 AA;
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es 7; Conserv
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NCBI_TaxID=1140;
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ID DVL2 XENLA

AC P51142;

DT 01-0CT-1996 ()

DT 15-MAR-2004 ()
                                                                                                             CHLD_SYNP7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                  CHID_SYNP7
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                                                                                         RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                        Segment polarity protein dishevelled homolog DVL-2 (Dishevelled-2) (DSH homolog 2) (Xdsh).
Kenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                    MEDLINE-58324391; PubMed-7600981; Sokol S.Y., Klingensmith J., Perrimon N., Itoh K.; Morensmith J., Perrimon N., Itoh K.; Moresalizing and neuralizing properties of Xdsh, a maternally expressed Xenopus homolog of dishevelled."; Development 121:1637-1647(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF6C9A1662DD7CEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wht signaling pathway, Developmental protein. DOMAIN 1 \ 82 \ \mathrm{DIX}.
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POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IRR000591; DEP.
InterPro; IRR000591; DEP.
InterPro; IRR000339; Dishevell.
InterPro; IRR003341; Dishevelled.
InterPro; IRR003441; Dishevelled.
InterPro; IRR001348; DIX.
InterPro; IRR001478; PDZ.
Pfan; PF00377; Dishevelled; 1.
Pfan; PF00579; DIX; 1.
Pfan; PF00595; PDZ; 1.
Pfan; PR00595; PDZ; 1.
Pfan; PR00785; DISHEVELLED.
PRINTS; PR01760; DISHEVELLED.
PRINTS; PR01760; DISHEVELLED.
PRINTS; PR003639; DIX; 1.
SWART; SM00049; DEP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U31552; AAB00688.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PS50186; DEP; 1.
PROSITE, PS50841; DIX; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                   Xenopodínae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; 151691; 151691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     680 (
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                      NCBI_TaxID=8355;
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428
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48.0%; Score 36; DB 1; Length 736;

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924 AA; 100253 MW; 0162C1591AF040AC CRC64;
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                                                                                                                                                                                        638 QDVVYLLREAIRR 650
                                                                                                                                           2 EKVQYLTRSAIRR 14
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                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesostigma viride.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                          RPOB MESVI
  SEQUENCE
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                                                                                                                                                                                                                                                             RESULT 23
RPOB_MESVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

-!-CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
-!-CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
-!-ENZWHE REGULATION: Hexokinase is an allosteric enzyme inhibited by its product Glc-6-P.
-!-SENDINI: Monomer.
-!-SENDINI: Monomer.
-!-COMAIN: THE N-AND C-TERMINAL HALVES OF THIS HEXOKINASE SHOW EXTENSIVE SEQUENCE SIMILARITY TO EACH OTHER. THE CATALYTIC ACTIVITY IS ASSOCIATED WITH THE N-TERMINUS WHILE REGULATORY FUNCTION IS ASSOCIATED WITH THE N-TERMINUS.
-!-MISCELLANEOUS: In vertebrates there are four major glucose-phosphorylating isoenzymes, designated hexokinase I, II, III and
                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                         Gaps
                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schwab D.A., Wilson J.E.; Complete amino acid sequence of the type III isozyme of rat hexokinase, deduced from the cloned cDNA."; Arch. Blochem. Biophys. 285:365-370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U73859; AAB18253.1; -.
HYSP; P05708; L13913.
HYSP; P05709; L183.
InterPro; IPR001312; Hexokinase.
Pfam; PF03727; hexokinase.
Pfam; PF03727; hexokinase; 2.
Pfam; PF03745; HEXOKINASE.
PRINTS; PR00475; HEXOKINASE.
PRODOM; PF00109; Hexokinase; 2.
PROSTIE; PS001109; HEXOKINASE; 2.
PROSTIE; PS00138; HEXOKINASES; 2.
Transferase; Kinase; Glycolysis; Allosteric enzyme; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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GLUCOSE-BINDING (POTENTIAL).
GLUCOSE-BINDING (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IV (glucokinase).
-!- SIMILARITY: Belongs to the hexokinase family.
                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
08-EPB-2003 (Rel. 41, Last annotation update)
Hexokinase type III (EC 2.7.1.1) (HK III).
  Pred. No. 69;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGULATORY.
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91378267; PubMed=1897938;
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                 624 EYSTRSSIRR 633
                                                                      5 OYLTRSAIRR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; Membrane.
DOMAIN 1 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [_TaxID=10116;
                                                                                                                                                                                                                                      HXK3 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCTION: DNA-dependent RNA polymerase catalyzes the transcription DNA into RNA using the four ribonucleoside triphosphates as
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beea', and beta'.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NIES-296;
MEDLINE-20150907; PubMed=10688199;
Lemteux C., Otis C., Turmel M.;
"Ancestral chloroplast genome in Mesostigma viride reveals an early branch of green plant evolution.";
Nature 403:649-652(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast.
Warayoca, Viridiplantae; Streptophyta; Mesostigmatophyceae;
Mesostigmatales; Mesostigmataceae; Mesostigma.
NCBL_TaxID=41882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.0%; Score 36; DB 1; Length 1080; 43.8%; Pred. No. 1e+02; 1ive 6; Mismatches 3; Indels
Query Match 48.0%; Score 36; DB 1; Length 924; Best Local Similarity 61.5%; Pred. No. 88; Matches 8; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                     PRT; 1080 AA
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STRANSBERGES, STAINSBERGES, STAINSBERGES, SARANSBERGES, SARANSBERGES, SCALLER, SCALLER, SCALLER, S. B. HOLL R.A., Evans C.A., Gocayne J.D., Adams N.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortnam J.R., Yango Q., Chen L.X., Amanatides P.G., Scherer S.E., Helf G., Nebbon L.X., Mixlos G.L.G., Brandon R.C., Baxter E.G., Helf G., Nebson C.R., Mixlos G.L.G., Abrill J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Bladdin D., Ballew R.M., Band R., Barder B.G., Borkeva D., Botchan M.R., Bauch M.R., Bander D., Botchan P., Botchan B.P., Borkeva D., Botchan M.R., Bauch M.R., Bander D., Botchar D., Chandra I., Botchar M.C., Borkeva D.A., Butler H., Cadieu E., Center A., Chandra I., An H.-J., Downes M., Dugan-Rocha S., Dunkov S., Dunkov S., Dunkov S., Dunkov B.C., Dunn P., Botchan M.C., Evangeliste C.C., Ferraz C., Ferriera S., Pleischman W., Gabrielina A.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Butris K.C., Evangeliste C.C., Ferraz C., Ferriera S., Pleischman W., Fornin M., Houston K.J., Bouns J., May M., Dugan-Rocha S., Dunkov B.C., Dunn P., An Harris N.L., Havardha T.J., Mai M.-H., Ibegam C.J., Kraft C., Kraft C., Kraft C., Kraft C., Kravitz S., Kulp D., Lai Z., Liasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Lidan Y., Lin X., Mattei B.E., Kodira C.D., Kraft C., Mortis J., Mosherson D., Noutt S.M., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L., Natleson D.K., Noutt S.M., Woy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L., Palazzolo M., Pithan G.S., Pan S., Pollard J., Puti, Y., Resee M.G., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stan B., Shout S., Shout S., Zhan M., Stang S., M., Wang Z.-Y., Wassarman D.A., Weinstender S., Cheeler F., Wassarman D.A., Weinstender S., Chuller S., Shon H., Schen S., Shon H., Shon R., Shon R., Shon R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
GG12740.
                                                                                                                                                                                 PRT;
66 LKRPKYNERISIRRAS 81
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                         RL28_DROME
                                                                                                              RESULT 24
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between

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                                                                                                                                                                                                                                                                                                     EMBL; AYO71444; AAL49066.1; -.
EMBL; AYO71444; AAL49066.1; -.
Flybase; FBERMO035422; CG12740,
GO; GO:0005842; CG12740;
GO; GO:0003735; F:structural constituent of ribosome; ISS.
GO; GO:0003735; P:structural constituent of ribosome; ISS.
InterPro; IPR003672; Ribosomal L28e;
Fam; PP01778; Ribosomal L28e;
ProDom; PD010767; Ribosomal L28e; 1.
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MEDLINE=99437995; PubWed=10508151;
O'Hara B.P., Norman R.A., Wan P.T., Roe S.M., Barrett T.E., Drew R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRUCKEL STRUCK N.A.
STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK N. STRUCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson S.A., Drew R.E., "Transcriptional analysis of the amidase operon from Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.7%; Score 35; DB 1; Length 144; 70.0%; Pred. No. 18; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 AA; 16029 MW; 14D5C7866P585113 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1989 (Rel. 11, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 177:3052-3057(1995).
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MEDLINE=95286483; PubMed=7539417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89211409; PubMed=2495988;
                                                                                                                                                                                                                                                                             EMBL; AE003477; AAF47742.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aliphatic amidase regulator.
AMIR OR PA3363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 70.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 LTRSAIRRAS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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P10932;
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                 EMBL, X13776; CAA32023.1; -.
EMBL, AE004758; AAG06751.1; -.
PIR, B83226; B8325.
PIR, S03884; S03884.
PDB, 1Q00, 23-DEC-99.
INTERPRO; IPR00556; ANTAR.
INTERPRO; IPR00561; ANTAR.
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ITMANSCIPPION regulation; Transcription antitermination; 3D-structure;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Sakaki Y., Hattori M., Omura S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MA-4680 / ATC 31267 / NCIMB 12804 / NRL 8165;
STRAIN=MA-4680 / ATC 31267 / NCIMB 12804 / NRL 8165;
MEDINE=2147403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hatcroff M.;
Genome. sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.7%; Score 41; DB 16; Length 116; 46.7%; Pred. No. 7.5; ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                           01.UUN-2003 (TrEMBLrel. 24, Created)
01.UUN-2003 (TrEMBLrel. 24, Last sequence update)
01.OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ribosomal protein L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                       PRT; 116 AA
                                                                                                                                                                                                                                              ALIGNMENTS
                    Q30735
Q81Y90
Q8YW51
Q92RY5
Q9NWF6
Q8C849
Q9AR53
Q9LVUI
Q82C01
  08PN39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces avermitilis.
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                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                      165
185
190
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Matches 7; Conserv
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444444444
6667
7.7.7.64444444
7.7.7.7.644
7.7.7.7.7.94
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  Query Match
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RESULT 2

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Fazeli C.F., Rezaian M.A.;

Fazeli C.F., Rezaian M.A.;

Fazeli C.F., Rezaian M.A.;

Fazeli C.F., Rezaian M.A.;

Fazeli C.F., Rezaian M.A.;

Fazeli C.F., Rezaian M.A.;

Fazeli C.F., Rezaian M.A.;

Fazeli C.F., Rezaian M.A.;

The genome of Grapevine leafroll-associated virus I and identification of three subgenomic RNAs.";

J. Gen. Virol. 81:605-615[2000].

EMBL, AF195822; AAF22738.1;

EMBL, AF195822; AAF22738.1;

GO, GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

GO, GO:0003509; P:Varal genome replication; IEA.

InterPro; IPR001788; RNA_dep_RNApol2.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Pyrococus abyssi genome sequence: insights into archaeal chromosome structure and evolution."; submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ248286; CAB49971.1; -
                                                                                                                                                                                                           Phospho-sugar mutase.
Pyrabiloslo OR PAB1666.
Pyrococcus abyssi.
Archaea, Buryarchaeota, Thermococci; Thermococcales, Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 AA; 49786 MW; F337BA57646E7269 CRC64;
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Last annotation update)
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        451 AA.
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                                                                                        Created)
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PROSITE, PS00710; PGM_PMM; 1.
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        PRELIMINARY;
                                                                                                                       01-MAY-2000 (TrEMBLrel. 01-JUN-2003 (TrEMBLrel.
                                                                                   01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=GES / Orsay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Q9UZTS
Q9UZTS;
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MEDLINE-98344137; PubMed=9679194; MEDLINE-98344137; PubMed=9679194; MEDLINE-98344137; PubMed=9679194; MEDLINE-98344137; PubMed=9679194; Mexarabayasi Y., Sawada M., Horikawa H., Hasoyama A., Nagai Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohluku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Makamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcacea; Pyrococcus.
                                                         Score 40; DB 16; Length 1104;
Pred. No. 1.3e+02;
6; Mismatches 2; Indels C
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        Hypothetical protein; Complete proteome. SEQUENCE 1104 AA; 125574 MW; 61C89EE3AB30C5DD CRC64;
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TIGREAMS; TIGRO1445; intein_Nterm; 2.

PROSITE; PS50813; INTEIN C_TER; 2.

PROSITE; PS50817; INT.N_TER; 2.

PROSITE; PS50817; INT.N_TER; 2.

PROSITE; PS50817; INT. 3.

Cell division; CompleTe proteome.

SEQUENCE 1108 AA; 125967 MW; 92D2578B31351F75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   058310,
01-AUG-1998 (TrEMBLrel. 07, Created)
01-CAN-1999 (TrEMBLrel. 09, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
1108AA long hypothetical cell division control protein.
                                                                                                                                                                                                                                                  PRT; 1108 AA.
                                                           53.3%;
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853 LSKIEHITPSAVRR 866
                                                                                                                            1 MEKVOYLTRSAIRR 14
                                                       Query Match
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus horikoshii.
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Best Local Similarity
Matches 8; Conserv
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STRAIN-RIMD 2210633 / Serctype O3:K6;

MEDINE-22506454; PubMed=12620739;

MAKID K., OSHima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

Lancet 361:743-749(2003).

EMBL; AP005088; BAC62605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                    Score 40, DB 12; Length 527;
Pred. No. 59;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC015626; AAH13626.1;
InterPro, IPR008160; Collagen.
Pfam; PF01391; Collagen, 12.
Hypothetical protein.
                                                                               SEQUENCE 527 AA; 59276 MW; C445CE1169B46132 CRC64;
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                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                            PRT; 998 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Breast tumor;
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PSvir.
Pfam, PF00978; RNA_dep_RNApol_2; 1.
RNA-directed RNA_polymerase.
                                                                                                                      53.3%;
80.0%;
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974 METIQWISRSTLKR 987
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Best Local Similarity 42.5.
Conservative
6: Conservative
                                                                                                                                     Best Local Similarity 80.0
Matches 8; Conservative
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SEQUENCE
                                                                                                                    Query Match
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Q8CFM4
ID Q8CFI
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Score 39; DB 16; Length 406;
Pred. No. 70;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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                  52.0%;
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Matches 8; Conservative
Query Match
Best Local Similarity 75.v
                                                                                                                                                273 KKÓVĽTŘEÁIŘŘ 284
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                                                                                                     3 KVOYLTRSAIRR 14
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NCBI_TaxID=29292;
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STRAIN=SF370 / ATCC 700294 / Serotype M1;
STRAIN=SF370 / ATCC 700294 / Serotype M1;
STRAIN=21192649; PubMed=11296296;
Ferretti J.G., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., McLaughlin R.;
Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
BMBL, AR006512, AAX3342.1; ---
BMBL, AR006512, AAX3342.1; ---
SEQUENCE 364 AA; 41754 MW; 038B8D36F4234020 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nelson K.E. weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Natins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Barins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolnay J., Madupu R., Nelson W., White Co., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzaz A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lubber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Fiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas putida (strain KT2440).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
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53.8%; Pred. No. 62; 3; Indels
tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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406 AA; 47318 MW; 7CDBC3ODF0D3C6E2 CRC64;
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Last annotation update)
                                                                                                                                                         01-JUN-2001 (TrEMBirel. 17, Created)
01-JUN-2001 (TrEMBirel. 17, Last sequence update)
01-DEC-2001 (TrEMBirel. 19, Last annotation update)
EPY0549.
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MEDLINE=22423060; PubMed=12534463;
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NCBI_TaxID=160488;
                                                668 MEVKDYLTREEVRKA 682
         1 MEKVQYLTRSAIRRA 15
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1314;
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SEQUENCE 40
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Gaps
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Besulfovibrio desulfuricans.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Desulfovibrio.
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"[Fe] hydrogenase of Desulfovibrio desulfuricans G20.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF331719; AAKI1625.1; --
HSSP; p00193; IDUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO: 0005489; F:electron transporter activity; IEA. GO; GO: 0006118; P:electron transport; IEA. InterPro; IPR001450; 4Fe45 ferredoxin.
InterPro; IPR001450; 4Fe45 ferredoxin.
InterPro; IPR001450; Fe hydrog.
Pfam; PF00037; fer4; 2. hyd_lg_C.
Pfam; PF00037; fer4; 2. hyd_lg_C.
Pfam; PF00037; fer4; 2. hyd_lg_C.
Pfam; PF02306; Fehyd_lg_C; 1.
PR0511E; PS00119; Fehyd_FERESDOXIN; 2.
FF6-45; IROM; IROM: SUBJECT ARA; 46120 MW; 1116557AB0C94219 CRC64;
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PYRAB04950 OR PAB0334.
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                                                           Smith D.R., Dougette-Ctamm L.A., DeLoughery C., Lee H.-M., Dubois Aldredge T., Bachirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Kaang Y., Lumm W., Pothlar B., Odu D., Spadadora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum J. Bacteriol. 179:7135-7155 (1997).
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G0; G0:0005874; C:microtubule; IEA.

G0; G0:0005129; F:GTP binding; IEA.

G0; G0:0007018; F:structural molecule activity; IEA.

G0; G0:0007018; P:microtubule-based movement; IEA.

InterPro; IPR00245; Beta tubulin.

PROSITE; PS00228; TUBULIN B AUTOREG; 1.

Hypothetical protein, Complete proteome.

SEQUENCE 119 AA; 13045 MW; D85119ED7630F098 CRC64;
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Pred. No. 30;
5; Mismatches 3;
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Sulfolobus tokodaii
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Q974N9;
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MEDLINE=22555397; PubMed=12674476;
MEDLINE=22559397; PubMed=12674476;
Kloetzel J.A., Barcin-Tourancheau A., Miceli C., Barchetta S.,
Farmar J., Banerjee D., Fleury-Aubusson A.;
"Plateins: a novel family of signal peptide-containing articulins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Kloetzel J.A., Baroin-Tourancheau A., Miceli C., Barchetta S.,
Farmar J., Banerjee D., Fleury-Aubusson A.,
"Cytoskeletal proteins with N-terminal signal peptides: plateins in
the ciliate Euplotes define a new family of articulins.";
J. Cell Sci. 116:1291-1303(2003).
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Euplotida; Euplotidae; Euplotes.
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Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                 52.0%; Score 39; DB 17; Length 481; 50.0%; Pred. No. 84;
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Pred. No. 1.1e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                      Indels
                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 481 AA; 55655 MW; 685FE30056A45259 CRC64;
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Last annotation update)
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01-JAN-1998 (TrEMBirel. 05, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
Hypothetical protein MTH425.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005267; F:potassium channel activity; 1
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPR001622; K+channel_pore.
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EMBL; AY124991; AAM94464.1; -.
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74972 MW;
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Best Local Similarity 54.5%;
Matches 6; Conservative
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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SEQUENCE FROM N.A.
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2 EKVQYLTRSAIRRAS 16
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
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nes 6, Conservative
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                                     PRELIMINARY;
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NCBI_TaxID=1314;
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Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005955; BAC50746.1; -.
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                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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EMBL; BX294147; CAD78621.1; -
Kinase; Transferase; Comple proceome.
SEQUENCE 211 AA; 23976 MW; 2FF54BF18F094376 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Thwiddine kinase Tdk (EC 2.7.1.21).
TDK OR RB8399.
Rhodopirellula baltica.
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                                              208 AA
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                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                              Bradyrhizobium japonicum.
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Best Local Similarity
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MEDLINSE-1192664; PubMed=11296256;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Vuan X., Clifton S.W., Ron B.A., McLaughlin R., Complete genome sequence of an M1 strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

GO, GO:0005737; C:cytoplasm, IEA.

GO, GO:0005737; C:cytoplasm, IEA.

GO, GO:000549; P:coproporphyrin piosynthesis; IEA.
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Wendland J., Philippsen P.;
Wendland J., Philippsen P.;
"Isolation and characterization of the Ashbya gossypii BUD3 gene.";
"Isolation and characterization of the EMBL/GenBank/DDBJ databases.
EMBL; AF210625; AAG41241.1; -...
NON TER 252
                                                                                       Ashbya gossypii (Yeast) (Eremothecium gossypii).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Ashbya.
NCBI_TaxID=33169;
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Pred. No. 66;
4; Mismatches 1; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-JTN-2001 (TrEMBLrel. 17, Last sequence update)
01-JTN-2003 (TrEMBLrel. 24, Last annotation update)
Putative coproporphyrinogen III oxidase (EC 1.3.3.3.3)
HEMN OR SPY1040.
Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
STREET A SECTYPE MI;
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Interpro; IPR004559; HemN rel.
Interpro; IPR007197; Radical SAM.
Pfam; PF04055; Radical SAM; I.
SWART; SM00729; Blp3; I.
                                                                                                                                                                                                                                                                                                                                                                                         252 AA; 27793 MW;
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54.5%;
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Pfam; PF04055; Radical SAM; 1.
SEQUENCE 398 AA; 45841 MW; 669A0563D1206261 CRC64;
                                                    Query Match
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Q8K7R5;
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Matches
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STRAIN=SSI-1 / Serotype M3;
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
Hayashi H., Hamada S.,
"The genome of invasive Streptococcus pyogenes; a comparative analysis
of S. pyogenes SSI-1, SR370 and MGASB332.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-MGASB222 / Serctype M18;
STRAIN-MGASB222 / Serctype M18;
SMOOT U.C., Barbian K.D., Van Gompel U.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefe S.M., Porcella S.F.,
Sylva G.L., Sturdevant D.E., Ricklefe S.M., Porcella S.F.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serctype M18
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
BMBL, AE010030; AAL97657.1; -.
GO, GO:0005737; C:cytoplasm; IEA.
GO, GO:0004109; F:coproporphyrinogen oxidase activity; IEA.
GO: GO:0006779; P:porphyrin biosynthesis; IEA.
                                                                                                                                                                                                          Streptococcus pyogenes (serotype M18).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcas.
Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR004559; Hemn rel.
InterPro; IPR007197; Radical SAM.
Pfam; PF04055; Radical SAM; I.
TIGRFAMS; TICR00539; hemn rel; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 376 AA; 43093 MW; 7236F821EE82EEE5 CRC64;
                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative coproporphyrinogen III oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 398 AA
                                                                                                                        01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence
01-UTW-2003 (TrEMBLrel. 24, Last annotat:
Putative coproporphyrinogen III oxidase.
HEMN OR SPYMIS_1022.
                                                                                               PRT;
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||: | |||: | |
102 EKIAVLQRSAVNRIS 116
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                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                        Streptococcus.
NCBI_TaxID=186103;
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                                                                                             Q8P177
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                                                              RESULT 18
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                                                                      Gaps
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MBDLINE=22133808; Pubmed=12122206;
MBDLINE=22133808; Pubmed=12122206;
MBammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
"Gentlevert P.M., Musser J.M.,"
"Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Emergence...,

Eroc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).

Embl. AE04150, AAM79280.1,

EMBL. AE041150, AAM79280.1,

EMBL. AE041150, AAM79280.1,

GO: 00:0005737, C:cytoplasm, IEA.

GO: 00:0004109; F:coproporphyrinogen oxidase activity, IEA.

R GO: 00:0004109; F:coproporphyrinogen oxidase activity, IEA.

R GO: 00:0004109; F:coproporphyrinogen oxidase activity, IEA.

R InterPro; IPR004559; HemN rel.

R InterPro; IPR007197; Radical SAM.

F Edm; PF04055; Radical SAM.

F Edm; PF04055; Radical SAM.

F EMART; SM00729; Elp3; I.

R TIGRFAMS; TIGR00539; hemN rel; 1.

Complete proteome; Hypothetical protein.

Complete Proteome; Hypothetical protein.
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Match
50.7%; Score 38; DB 16; Length 39
Local Similarity 53.3%; Pred. No. 1.1e+02;
ies 8; Conservative 2; Mismatches 5; Indels
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Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes (serotype M3).
Bacteria, Firmicutes; Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus agalactiae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Putative coproporphyrinogen III oxidase.
HEMN OR SPYM3_0673.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                              408 AA.
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                                                                                                                                                                                124 EKIAVLORSAVNRIS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 EKIAVLORSAVNRIS 148
                                                                                                                          2 EKVOYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EKVQYLTRSAIRRAS 16
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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related, matrix

PROSITE;

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Glocckner G., Eichinger L., Zaffranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Plarzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostellum discoideum."; Nature 418:79-85(2002).
                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OTN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to Homo sapiens (Human). similar to SWI/SNF related, matassociated, actin dependent regulator of chromatin, subfamily c,
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116989; AAM43749.2; -
EMBL; AC116989; AAM43749.2; -
EMBL; AC116989; AAM43749.2; -
EMBL; AC116989; AAM43749.2; -
EMBL; AC116989; MAP DIMA binding.
InterPro; IPRO01673; S mold repeat.
Pfam; PF00526; S mold repeat.
PFAMT; SM0017; SM014 repeat; 13.
SWART; SM0017; SM17 1.
PROSITE: PS50090; NYB 3; 1.
SEQUENCE 1223 AA; 136240 MW; B7D92E2925F39C72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.7%; Score 38; DB 5; Length 1223; 80.0%; Pred. No. 3.6e+02; ive 1; Mismatches 1; Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                               Dictyostellum discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
NCBI_TaxID=44689;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ferredoxin-dependent glutamate synthase.
GLSF OR TLL1368.
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Interpro, 1PR002932; Glu_synthase.
Interpro, 1PR006982; Glu_synth_centr.
                                                                                                                                                                                                                                                                                                                                                     STRAIN=AX4;
MEDLINE=22092622; PubMed=12097910;
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nes 8; Conservative
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01-MAR-2003 (
01-MAR-2003 (
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                  Lachenauer C.S., Creti R., Michel J.L., Madoff L.C.;
"Mosaicism in the alpha-like protein genes of group B streptococci.";
Proc. Natl. Acad. Sci. U.S.A. 97:9630-9635 (2000).
-i- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIM-C.N. Nipponbare;
Buell C.R., Yann Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Buell C.R., Taitrin T., Kim M.M., Bera J.J., Jin S.S.,
Overton II L.L., Tsitrin T., Koo H., Zismann V., Haiso J., Blunt S.,
Vandken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang O.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
Mite O., Salzberg S.L., Fraser C.M.,
Mite O., Salzberg S.L., Fraser C.M.,
Mite O., Salzberg S.L., Fraser C.M.,
Mite O., Balzberg S.L., Sub B.B., Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         EMBL, AF248638; AAG09976.1; -..
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006355; P:regulation; IEA.
InterPro; JER001034; HTH_DEOR.
Pfam; PF00455; deoR; I.
SMART; SM00420; HTH_DEOR; I.
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56.2%; Pred. No. 2.5e+02;
tive 2; Mismatches 5; Indels
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E; PS00894; HTH DEOR FAMILY; 1.
nding; Transcription; Transcription regulation.
CE 578 AA; 66770 MW; CIDE74FB5943B8E3 CRC64;
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SEQUENCE 882 AA; 96573 MW; SCDCB01A2569CEC0 CRC64;
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      MEDLINE=20402586; PubMed=10944228;
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SEQUENCE 57
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MEDLINE-22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Back A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
Complete genome sequence of the marine planctomycete Pirellula sp.
strain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
EMBL; BR294136; AD72339.11.
Hypothetical protein; Complete protecome.
SEQUENCE 68 AA: 7494 MW; 7ECIFDP98DBSF67C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Rhodopirellula baltica.
Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales,
Planctomycetaceae, Pirellula.
NCBL_TaxID=117;
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50.7%; Score 38; DB 16; Length 1541;
Best Local Similarity 53.3%; Pred. No. 4.6e+02;
Matches 8; Conservative 2; Mismatches 5; Indels C
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InterPro; IPR006981; Glu_synth_NTN.
Pfam; PF01645; Glu_synthhase; 1.
Pfam; PF04899; Glu_synth NTN; 1.
Pfam; PF04899; Glu_synt Central; 1.
Pfam; PF04499; GXGXG; 1.
Complete proteome: A 168017 MW; 9CB26077859306A6 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Created)
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|           | Score          | 76                 | 76                 | 76                 | 76                 | 71       | 71                 | 71       | 71                 | 7.1                | 71                 | 71                 | 71                 | 71       | 71                 | 71                 | 71                 | 71                 | 71       | 68                 | 68                 | 67                 | 99                 | 65                 | 62                 | 42                 |
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Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a, cardiant; cardiamycoyre; transport peptide; penetratin; cargo peptide; contractilin; cargo contractility; inhibitor; cardiac disease; mutant; treatment; heart failure; mycoardial dysfunction; recombinant protein;
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                                                                                                                                                                                                                                                                                                                              Penetratin-based recombinant phospholamban peptide, TAT-mutant PLB.
                                                                                       ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus.
       Q 4
                                                                                                                                                                                                                                                                                      29-AUG-2000 (first entry)
       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAT protein.
    46.1
46.1
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       35
                                                                                                                                                                                                                                              AAY71014;
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                                                                                                                                                         RESULT 1
                                                                                                                                                                              AAY71014
    99
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Hoshijima M, Meyer M;
                                                                               /note= "Wild type Ser replaced with Glu"
                                                                                                                            не н,
                                                                                                                            Minamisawa S,
                                                                                                                               Wang Y, Silverman GJ;
                                                                                                               99US-0145883P.
                                                                                                           98US-0106718P.
                                                                                                    99WO-US025692
                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                            Dillman W,
                                                                                                                                      WPI; 2000-365393/31.
                                                                                      WO200025804-A2
                                                                                                    02-NOV-1999;
                                                                                                           02-NOV-1998;
                                                                                                               27-JUL-1999;
                                                                                                                            Chien K,
Scott C,
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Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Example 5; Page 53; 56pp; English.

small peptide complexes may recombine that induces that induces phospholambar (FLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ArPase (SERCA2a) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin. PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinant peptide TAT-mutant PLB, comprising the amino terminal end of human PLB mutant (Ser31Glu) protein, attached to the 3' end of denatured human immunodeficiency virus (HIV), TAT protein. Penetratin is a class of The patent discloses a method for the treatment of heart failure, using

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                                                                                                                                                                                                                                                                                                                                                                              Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit [ily; ANT; antennapedia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCAZa) within cardiomycoytee. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a method for the treatment of heart failure, using

    .20
/note= "Corresponds to mutant human phospholamban (PLB)
amino terminal peptide"

                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Corresponds to Drosophila antennapedia (ANT) transport peptide"
peptides, with translocating properties having the ability to carry hydrophilic compounds across the plasma membrane
                                                                                                                                                                                                                                                                                                                                                     Penetratin-based recombinant phospholamban peptide, mutant PLB-ANT.
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                                                                                                              0
                                                                                 Length 35,
                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild type Ser replaced with Glu"
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                                                                              100.0%; Score 76; DB 3; I
100.0%; Pred. No. 2.2e-06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                          AAY71013 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Page 53; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0106718P.
99US-0145883P.
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                                                                                                                                               1 MEKVQYLTRSAIRRAE 16
                                                                                                                                                                            16 MEKVOYLTRSAIRRAE 31
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                              Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21. .36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-365393/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 16
                                                 Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200025804-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1999;
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Scott C,
                                                                                                                                                                                                                                                                                         AAY71013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to delivering a therapeutic dose of a gene expression cassette in a fluid selectively to heart for sustained expression, comprising employing a viral vector together with a vascular permeabilising agent. The method is useful for gene therapy delivering genes for improving or enhancing cardiac function, particularly in hamster models of heart disease. The present sequence is that of a pseudophosphorylation mutant of phospholamban (SiGEPLB). This point mutant is among a number of dominant negative mutants identified and characterised in WOOO/25804 and used in the method of the present
dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinate peptide, mutant PLB-ANT, comprising the amino terminal end of human PLB mutant (Ger16Glu) protein, attached to the 5' end of the Drosophila antennapedia (ANT) transport peptide. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; phospholamban; PLB; cardiant; heart disease; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 76; DB 3; Length 36; 100.0%; Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human phospholamban pseudophosphorylation mutant S16E PLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wildtype Ser substituted by Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Fig 1; 12pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB79404 standard; peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEKVOYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2001; 2001US-00954571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-2000; 2000US-0231821P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEKVOYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chien KR, Hoshijma M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-361185/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HOSH/) HOSHIJMA M.
(ROSS/) ROSS J.
(IKED/) IKEDA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIE/) CHIEN K R.
                                                                                                                                                                                                                                                                                                                                                         Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002032167-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB79404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                         Phospholamban, PLB; human, sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiamt, cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; mutant, treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum (22 2+ Arpase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                H6 tagged penetratin-based recombinant protein, H6-(S16E)mutantPLB-ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Corresponds to mutant human phospholamban (PLB)
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63. 78
/note= "Corresponds to Drosophila antennapedia (ANT)
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e= "Corresponds to hexahistidine tag (H6)"
                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Wild type Ser replaced with Glu"
                                                    Score 76; DB 5; L
Pred. No. 3.4e-06;
                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V. Minamisawa S,Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transport peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 55; 56pp; English.
                                                                                                                                                                                                              AAY71018 standard; protein; 79 AA.
                                                    100.0%; Sc
100.0%; Pr
tive 0;
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99US-0145883P.
                                                                                                            1 MEKVQYLTRSAIRRAE 16
                                                                                                                                      1 MEKVOYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                      29-AUG-2000 (first entry)
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365393/31.
                                                    Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                          Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200025804-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Drosophila sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
invention
                                                                                                                                                                                                                                          AAY71018;
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Scott C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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                                                                                                                                                                                  RESULT 4
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cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractions). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCACA interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and mycocardial dysfunction. The present sequence is the hexahistidine (HB) tagged penetratin-based recombinant protein H6-mutantishidine (HB) tagged human mutant (Sarl6dul) PLB protein and brosophila antennapedia (ANT) transport peptide attached by a hexahistidine tag. This sequence is
            888888888888
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Sequence 79 AA;

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0; Gaps
  Length 79;
Match 100.0%; Score 76; DB 3; Length 79 Local Similarity 100.0%; Pred. No. 5.2e-06; Los 16; Conservative 0; Mismatches 0; Indels
      Query Match
                                          Matches
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1 MEKVOYLTRSAIRRAE 16 용 ð

1 MEKVQYLTRSAIRRAE 16

AAY71009 standard; peptide; 16 AA. 29-AUG-2000 (first entry) RESULT 5 

Human Phospholamban (PLB) cargo peptide.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SBRCA2a; cardiant; cardiamyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction.

Homo sapiens.

WO200025804-A2.

11-MAY-2000.

02-NOV-1999;

98US-0106718P. 02-NOV-1998; 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

Hoshijima M, Meyer M; He H, Chien K, Dillman W, Minamisawa S, Scott C, Wang Y, Silverman GJ;

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase

Example 4; Page 50; 56pp; English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum (2 + Arbase (SRRCA2a) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the cargo peptide from

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                                                                                                                                                                                                                                                                                                                                                                                                                        Phospholamban, PLB, human, sarcoplasmic reticulum Ca 2+ ATPase, SERCA2a, cardiant, cardiadomyocyte; transport peptide, penetratin, cargo peptide, contractilin, cardiac contractility, inhibitor, cardiac disease, treatment; heart failure, myocardial dysfunction, recombinant peptide,
human PLB amino terminal residues 1-16. It could be derived from any segment of wild type or mutant PLB protein. The cargo peptide is linked to the transport peptide by a covalent linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5..15 /note= "Corresponds to denatured human immunodeficiency virus (HIV) TAT protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Corresponds to human phospholamban (PLB) amino
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   He H, Hoshijima M, Meyer M;
                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                           Penetratin-based recombinant phospholamban peptide, TAT-PLB.
                                                                                                   Length 16;
                                                                                                   93.4%; Score 71; DB 3; Le
100.0%; Pred. No. 7.6e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillman W, Minamisawa S, Wang Y, Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 52; 56pp; English.
                                                                                                                                                                                                                                                                                         AAY71012 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terminal peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0145883P.
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                                                                                                                                                                      1 MEKVOYLTRSAIRRA 15
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                      15; Conservative
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                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; TAT protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       triphosphatase.
                                                                    Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-1999;
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Scott C,
                                                                                                     Query Match
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contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinant peptide TAT-PLB, comprising the amino terminal end of human PLB native protein, attached to the 3' end of denatured human immunodeficiency virus (HIV), TAT protein. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cardio peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; recombinant peptide; fruit fly; antennapedia; ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Corresponds to human phospholamban (PLB) amino
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penetratin-based recombinant phospholamban peptide, PLB-ANT.
                                                                                                                                                                                                                                                                                                      Length 35;
                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                      93.4%; Score 71; DB 3; Li
100.0%; Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                        100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71011 standard, peptide; 36 AA
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99US-0145883P.
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                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEKVOYLTRSAIRRA 15
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                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                              plasma membrane
                                                                                                                                                                                                                                                       Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200025804-A2
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Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                          He H, Hoshijima M, Meyer M;
                                                          Minamisawa S,
                                                                                                                                                                                                                                                                                                                                            Example 5; Page 52; 56pp; English.
                                                                                Wang Y, Silverman GJ;
(REGC ) UNIV CALIFORNIA.
                                                       Dillman W,
                                                                                                                                          WPI; 2000-365393/31.
                                                                                                                                                                                                                                                                                        triphosphatase.
                                                       Chien K,
Scott C,
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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, SERCA_2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
and sarcoplasmic reticulum Ca 2+ AFPase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinant epptide PLB-ANT, comprising the amino terminal end of human PLB native protein, attached to the 5, end of the Drosophila antennapedia (ANT) transport peptide. Penetratin is a class of peptides, with translocating properties, having the ability to carry hydrophilic compounds across the
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            ö,
                                                                                                                                                                                                                                                                                                          Length 36,
                                                                                                                                                                                                                                                                                                                                            0; Indels
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tta T, Kaivola
                                                                                                                                                                                                                                                                                                      93.4%; Score 71; DB 3; Lv 100.0%; Pred. No. 1.8e-05; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tenhunen J, Vrustan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 9; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE45175 standard; peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                       1 MEKVQYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                 1 MEKVOYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                  (first entry)
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Yliperttula-Ikonen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-019625/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORIN ) ORION CORP.
                                                                                                                                                                                                                                                                   Sequence 36 AA;
                                                                                                                                                                                                                               plasma membrane
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site comprises Met-20, Lys-27 and/or Leu-28, and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzoly. 5,7-bis ((IH-tetrazol-5-yl)-methyloxy)-4-methyl-2H-methyl-2H-1-benzopyzan-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2 + -ATPase. The compound is useful for reliaving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phospholamban, PLB, human, sarcoplasmic reticulum Ca 2+ ATPase, SERCA2a, cardiant, cardiomyocyte; transport peptide; penetratin, cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                            93.4%; Score 71; DB 8; Length 36; 100.0%; Pred. No. 1.8e-05; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mutant phospholamban (PLB) S16N protein.
                                                                                                                                                                                                                                                                  cytosolic domain of human phospholamban.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 Sequence 36 AA;
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dominant negative inhibitor of PIB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PIB protein, comprising the mutation Serieban. This mutant sequence when overexpressed in the transformed cardiomyocytes, shows increased contractility than the wild type PIB sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phospholamban, PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a, carddant; carddomyocytre; transport peptide; penetratin, cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                93.4%; Score 71; DB 3; Length 52; 100.0%; Pred. No. 2.7e-05;
                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                           100.0%; Preq. ...
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                                                                                                                                                                                                                                                                                                                                                                               AAY71003 standard; protein; 52 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-365393/31.
                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                Sequence 52 AA;
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Scott C,
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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (plB) deficiency and inhibits the interaction between PlB and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2s) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PlB, native PlB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting Interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine

Disclosure, Page 49; 56pp; English.

triphosphatase.

Hoshijima M,

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Minamisawa Silverman GJ;

Dillman W,

Chien K, Scott C,

Wang Y,

WPI; 2000-365393/31.

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treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising a sense mutation Val49Ala. This mutant sequence when overexpressed in the transformed cardiomyocytes, shows increased contractility than the wild type PLB sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant, cardiamyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Transmembrane sector made of uncharged residues responsible for stabilising the pentamer formation"
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    20
/label= Domain_Ia
    Moote= "Rich in alpha-helical confirmation with a net
positive charge"

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                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                 93.4%; Score 71; DB 3; Length 52; 100.0%; Pred. No. 2.7e-05; live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Phospholamban (PLB) wild type protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY71002 standard; protein; 52 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0106718P.
99US-0145883P.
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                                                                                                                                                                                                                                                                                                                                                                                    1 MEKVOYLTRSAIRRA 15
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                                                                                                                                                                                                                                               Local Similarity 100. Les 15; Conservative
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                                                                                                                                                                  Sequence 52 AA;
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Scott C,
                                                                                                                                                                                                                    Query Match
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and sarcoplasmic reticulum Ca 2+ ATPase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PiB, native PiB or antibody against PiB protein (contractilin). Penetratin-PiB peptide functions as a dominant negative inhibitor of PiB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myccardial dysfunction. The present amino acid sequence is the human PiB wild type protein, a potent inhibitor of SERCA2a activity. It primarily exists in a pentaneric form. It is a mediator in the regulation of myocardial function by catecholamines through the cAMP cascade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes substantially purified human proteins treferred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ARNISTS2 and ARNISTS2 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manifacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX planting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psortiasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hyperternaton; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; inflectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                                                                                                                                                                                  93.4%; Score 71; DB 3; Length 52; 100.0%; Pred. No. 2.7e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORFX protein sequence SEQ ID NO:13166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP06592 standard; protein; 52 AA.
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29-AUG-2000; 2000US-0228716P.
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                                                                                                                                                                                                                                                                                                                                         15; Conservative
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                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                            Sequence 52 AA;
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sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, operials, benign tumours, keloid, degenerative disorders haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease, autoimmune thilammatory eve disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from respectusion injury in various tissues and conditions resulting from form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pot\_sequences

8566666666666666666888

Seguence 52 AA;

0; Gaps Length 52; 0; Indels 93.4%; Score 71; DB 5; Le 100.0%; Pred. No. 2.7e-05; tive 0; Mismatches 0; 1 MEKVOYLTRSAIRRA 15 1 MEKVOYLTRSAIRRA 15 Conservative Similarity Ma. Local b. 15; Query Match Matches ò 8

RESULT 13

ADE45172 standard; protein; 52 AA. ADE45172

ADE45172;

29-JAN-2004 (first entry)

Mouse SERCA\_2 inhibitor phospholamban.

Mouse, SERCA\_2, phospholamban, PLB, Ca2+ ATPase of the sarco/endoplasmic reticulum, protein co-ordinate data, cardiant.

US6538022-B1.

25-MAR-2003.

99US-00252063 18-FEB-1999; 97US-00937117 24-SEP-1997;

(ORIN ) ORION CORP.

Ovaska M, Tenhunen J, Vidgren  $J_i$  onen M, Tilgmann C, Lotta T, Kaivola  $J_i$ Yliperttula-Ikonen M, Pollesello P,

WPI; 2004-019625/02.

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+ ATPase.

Claim 1; SEQ ID NO 6; 65pp; English.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (FIB) protein (an inhibitor of SRCA\_2, Ca2+ AIPase of the sarco/endoplesmic reticulum ) appearing as ADB45167-ADB45173. The compound has a structure containing three of the four moleties: an electronegative molety associating with an SI binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative 

moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site comprises Arg-14; a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is not 3-berzyl-5,7-bis ([HH-tetrazol-5-y1)-methyloxy)-4-methyl-2H-methyl-2H-l-benzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca. 2 + -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA\_2. The present sequence is a phospholamban. 88888888888888888

Sequence 52 AA;

0; Gaps 93.4%; Score 71; DB 8; Length 52; 100.0%; Pred. No. 2.7e-05; tive 0; Mismatches 0; Indels 15; Conservative Similarity Query Match Best Local

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RESULT 14

ADE451

ADE45170 standard; protein; 52 AA. ADE45170;

(first entry) 29-JAN-2004 Rabbit SERCA\_2 inhibitor phospholamban.

Rabbit; SERCA 2; phospholamban; PLB; Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data; cardiant. 

Oryctolagus cuniculus.

US6538022-B1

25-MAR-2003.

18-FEB-1999;

97US-00937117. 24-SEP-1997;

99US-00252063.

(ORIN.) ORION CORP.

Pollesello P, Ovaska M, Tenhunen J, Vidgren J; Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;

WPI; 2004-019625/02.

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+ -ATPase.

Claim 1; SEQ ID NO 4; 65pp; English.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, Ca2+ Arpense of the sarco/endoplasmic reticulum) appearing as ADE45167-ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site comprises Arg-14; a hydrophobic moiety associating with an S3 binding site comprises Arg-14; a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding

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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA, 2, Ca2+ ArPase of the sarco/endoplasmic reticulum, appearing as ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB45167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB5167-ADB516
site comprises Met-20, Lys-27 and/or Leu-28, and a hydrophobic moiety associating with an S4 binding site of the phospholamban cycosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzyl-5,7-bis ((IH-tetrazol-5-yl)-methyloxy)-4-methyl-2H-methyl-2H-benzopyran-2-one. Also included are deactivating thospholamban, comprising administering the novel compound to stimulate the Ca 2 + -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; SERCA 2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
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                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                        93.4%; Score 71; DB 8; Length 52; 100.0%; Pred. No. 2.7e-05; 1ve 0; Mismatches 0; Indels
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onen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat SERCA_2 inhibitor phospholamban.
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Yliperttula-Ikonen M,
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Best Local Similarity
....hes 15; Conserva
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                                                                                                                                                                                                                                                                                          Sequence 52 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiant.
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Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
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stimulating Ca2+
-methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2 + -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sl binding site residue claimed in claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "S3 binding site residue claimed in claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "S3 binding site residue claimed in claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "S1 binding site residue claimed in claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "S3 binding site residue claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "S2 binding site residue claimed in
                                                                                                     93.4%; Score 71; DB 8; Length 52; 100.0%; Pred. No. 2.7e-05; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New compound, useful for relieving inhibitory effects of cardiac SR Ca2+-ATPase by deactivating phospholamban and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4, Tenhunen J, Vidgren J;
Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "S1 binding site residue claimed
                                                                                                                                                                                                                                                                                                                                 Human SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1; 65pp; English
                                                                                                                                                                                                                                                   ADE45167 standard; protein; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00937117.
                                                                                                                                                          1 MEKVQYLTRSAIRRA 15
                                                                                                                                                                                 1 MEKVOYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                         29-JAN-2004 (first entry)
                                                                                                                  Local Similarity 100, 1es 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pollesello P, Ovaska M, Yliperttula-Ikonen M, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORIN ) ORION CORP.
                                                                             Sequence 52 AA;
                                                    phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding-site
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                                                                                                                                                                                                                                                                              ADE45167;
                                                                                                                                                                                                                                                                                                                                                                                      cardiant.
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATPase.
                                                                                                                                  Matches
                                                                                                                                                                                                                          RESULT 16
                                                                                                                                                                                                                                         ADE45167
 8x8383888
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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, 224. ATPBase of the sarco/endoplasmic reliculum ) appearing as ADB45167-ADB4513. The compound has a structure containing three of the four moiettes: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is not 3-benzyl-5,7-bis ((IH-tetrazol-5-yl)-methyloxy)-4-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyloxyl-4-methyl-2H-methyl-2H-methyl-2H-methyloxyl-4-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-methyl-2H-meth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phospholamban, PLB; human, sarcoplasmic reticulum Ca 2+ ATPase, SERCA2a, cardiant, cardiomycorpe, transport peptide, penetratin, cargo peptide, contractilin, cardiac contractility; inhibitor; cardiac disease; mutant, treatment; heart fallure; myccardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H6 tagged penetratin-based recombinant protein, H6-(V49A) mutantPLB-ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Corresponds to mutant human phospholamban (PLB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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/note= "Corresponds to Drosophila antennapedia (ANT)
transport peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .58
.e= "Corresponds to hexahistidine tag (H6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.4%; Score 71; DB 8; Length 52; 100.0%; Pred. No. 2.7e-05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Wild type Val replaced with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY71019 standard; protein; 79 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
Drosophila sp.
Synthetic.
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27-JUL-1999;
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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB can discretion between PLB and sarcoplasmic reticultum Ca 2+ ATPaca (SERCAZA) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against CPLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCAZA interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the hexahistidine (H6) tagged penetratin-based recombinant protein H6-mutantPLB-ANT, comprising the human mutant (Val49Ala) PLB protein and brosophila antennapedia (ANT) transport peptide attached by a hexahistidine tag. This sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Corresponds to Human phospholamban (PLB) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
                                                                                                                                     Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hexahistidine tagged penetratin-based recombinant protein, H6-wtPLB-ANT.
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/note= "Corresponds to Drosophila antennapedia (ANT)
transport peptide"
                                                  Meyer M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.4%; Score 71; DB 3; Length 79; 100.0%; Pred. No. 4.2e-05; ive 0; Mismatches 0; Indels
                                                  Hoshijima M,
                                                  Не н,
                                                Dillman W, Minamisawa S,
Wang Y, Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                 Example 6; Page 56; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71017 standard; protein; 79 AA.
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Best Local Similarity 100.(
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53. .58
/note= "C
               (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                       WPI; 2000-365393/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 79 AA;
                                                                                                                                                                                              triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
Drosophila sp.
Synthetic.
                                                Chien K,
Scott C,
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig; SERCA_2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                   Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                He H, Hoshijima M, Meyer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                93.4%; Score 71; DB 3; Length 79; 100.0%; Pred. No. 4.2e-05; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                            Example 6; Page 54-55; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pig SERCA_2 inhibitor phospholamban.
                                                                                                Minamisawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE45168 standard; protein; 52 AA.
                                                                                                          Wang Y, Silverman GJ;
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                                         98US-0106718P.
99US-0145883P.
                      99WO-US025692
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                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                              Dillman W,
                                                                                                                                 WPI; 2000-365393/31.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORIN ) ORION CORP.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 79 AA;
                                                                                                                                                                                        triphosphatase.
                     02-NOV-1999;
                                         02-NOV-1998;
27-JUL-1999;
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11-MAY-2000
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                                                                                                Chien K,
                                                                                                          Scott C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an imhibitor of SERCA 2, Ca2+ ATPase of the sarco/endoplasmic reticulum ) appearing as ADB45167-ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyre, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound, the S2 binding site of the phospholamen cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban comprises the compound is not 3-benzyl-5/-bis ([1H-tetrazol-5-yl])-methyloxyl-4-methyl-2H-methyl-2H-methyl-2H-benzopyran-2-one. Also included are deactivating the case of the case of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                  New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dog; SERCA_2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Ovaska M, Tenhunen J, Vidgren J;
onen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pollesello P, Ovaska M, Tenhunen J, Vidgren J;
Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dog SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE45169 standard; protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00252063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDKVQYLTRSAIRRA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 93.3
nes 14; Conservative
                                        Yliperttula-Ikonen M,
                                                                                                             WPI; 2004-019625/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ORIN ) ORION CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phospholamban.
        Pollesello P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6538022-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiant
                                                                                                                                                                                                                                                                   -ATPase.
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New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
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onen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chicken SERCA_2 inhibitor phospholamban.
                                                                                                                                                                            Claim 1; SEQ ID NO 3; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE45173 standard; protein; 52 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDKVQYLTRSAIRRA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
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Yliperttula-Ikonen M,
WPI; 2004-019625/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-019625/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6538022-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE45173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiant.
                                                                                                                      ATPase.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, 22.4 ATPase of the sarco/endoplasmic reticulum of appearing as ADE45167-ADE4513. The compound has a structure containing three of the four moiettes: an electromegative moiety associating with an SI binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Azg-9 and/or Arg-13; an electromegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound, the S2 binding site of the phospholamban cytosolic comain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain the compound is bound, the binding site comprises Phospholamban, comprised the binding site comprises Phospholamban comprised the compound is not 3-benzyl-57-bis ((1H-tetrazol-5-4)) methyloxyl-4 methyl-2H-methyl-2H-methyl-2H-lenzopyzan-2-one. Also included are deactivating the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.2%; Score 67; DB 8; Length 52; 86.7%; Pred. No. 0.00014; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /hote= "Wild type Arg replaced with Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human mutant phospholamban (PLB) R14E protein.
                                                              Claim 1; SEQ ID NO 7; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71005 standard; protein; 52 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phospholamban.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
-ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                          New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
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Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.5%; Score 68; DB 8; Length 52; 93.3%; Pred, No. 9.3e-05; ive 1; Mismatches 0; Indels
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Gaps

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Meyer M;

Hoshijima M,

He H,

Chien K, Dillman W, Minamisawa S, Scott C, Wang Y, Silverman GJ;

WPI; 2000-365393/31.

99US-0145883P.

(REGC ) UNIV CALIFORNIA.

98US-0106718P

02-NOV-1998; 27-JUL-1999;

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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum C2 + Arpase (SERCA2a) within cardiomycorptes. The peptide complex comprises of transport peptide like penetrain and cargo peptide complex comprises of transport peptide like penetrain and PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising a sense mutation Argidulus, shows increased contractility than the wild type PLB sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardianycoyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.
               Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                         86.8%; Score 66; DB 3; Length 52; 93.3%; Pred. No. 0.00021; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human mutant phospholamban (PLB) E2A protein.
                                                                                                     Disclosure; Page 48-49; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY71004 standard; protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEKVOYLTRSAIRRA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                    triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52 AA;
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small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ Aprase (SERCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against pLB protein (contractilli). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myccardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the mutantion Glu2Ala. This mutant sequence when overexpressed in the transformed cardiomycoytes, shows increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating cardiac diseases, e.g. heart failure or myocardial dysfunction
                                                                                                     patent discloses a method for the treatment of heart failure, using
comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
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                                                                                                                                                                                                                                                                                                                                                                                                             85.5%; Score 65; DB 3; Length 52;
93.3%; Pred. No. 0.00032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild type Arg replaced with Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      He H, Hoshijima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human mutant phospholamban (PLB) K3E/R14E protein.
                                                                                                                                                                                                                                                                                                                                      contractility than the wild type PLB sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                     Disclosure, Page 48; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY71007 standard; protein; 52 AA.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 14
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 52 AA;
                                      triphosphatase.
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Scott C,
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He H, Hoshijima M,

Minamisawa S,

Dillman W, Minamisawa Wang Y, Silverman GJ;

Chien K, Scott C,

WPI; 2000-365393/31.

(REGC ) UNIV CALIFORNIA.

27-JUL-1999; 02-NOV-1998;

98US-0106718P 99US-0145883F

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comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.
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Disclosure; Page 49; 56pp; English.

small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (SRCA2a) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treament of cardiac disease e.g. heart failure and myccardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the double mutation lyssquance when overexpressed in the transformed cardiomycottes, shows increased contractility than the wild type PLB sequence The patent discloses a method for the treatment of heart failure, using 

Sequence 52 AA;

Gaps .. 81.6%; Score 62; DB 3; Length 52; 86.7%; Pred. No. 0.0011; live 1; Mismatches 1; Indels 1 MEKVQYLTRSAIRRA 15 Query Match Best Local Similarity 86.7% Matches 13; Conservative à 엄

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RESULT 25

ADC87928 standard; protein; 116 AA. ADC87928

01-JAN-2004 (first entry) ADC87928; 

Ribosomal protein similar to FCWP1 #144.

Macrophomina, Mycosphaerella; Nectria; Peronospora; Phoma; Pyphaerotrichum; Phycophthora; Plasmoppara; Podosphaera; Puccinia; Puthium; Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Scerotium; Sclerotinia; Septoria; Thielaviopsis; Venturia; Verticillium. plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora; Colletotrichum; Diplodia; Fusarium; Gaeumanomyces; Helminthosporium; Antifungal protein; ribosomal protein; FCWP1; AlyAFP;

Unidentified.

JS6573361-B1.

03-JUN-2003.

07-DEC-2000; 2000US-00732210.

99US-0169513P. 99US-0169340P. 07-DEC-1999; 07-DEC-1999; (MONS ) MONSANTO TECHNOLOGY LLC

Bunkers GJ, Liang J, Mittanck CA, Seale JW, WPI; 2003-754558/71. Novel antifungal protein FCWF1, isolated from Fusarium culmorum, useful for controlling fungal infections in plants.

Example 21; SEQ ID NO 181; 27pp; English.

The invention relates to an isolated antifungal ribosomal protein from

c rusarium Guimorum, F. Auso included is a "Histin protein between consider by the nucleic acid appearing as a ADG8775; The FVPP proteins are decoded by the nucleic acid appearing as ADG8775; The FVPP proteins are useful for controlling fungal infections in plants, such as those caused bacochyte (e.g. Amcorbyta pisi).

Ascochyta (e.g. Amcorbyta pisi); Botrytis (e.g. Botrytis cinerea), cercospora (e.g. Amcorbyta pisi); Botrytis (e.g. Botrytis cinerea), collectrichum inclementalaum ). Diplodia (e.g. Bacchyta pisi); Botrytis (e.g. Botrytis cinerea), collectrichum inclementalaum of plantium carganium plastium genarium quantum plastium genarium quantum plastium genarium quantum plastium genarium carbonum in elegarium genarium solani; Fusarium genarium carbonum in elegarium genarium carbonum in elegarium genarium genarium carbonum in elegarium genarium plastium genarium genarium genarium maydis ), Morcophomina (e.g. Macrophomina phaseolia, Metria (Nectria hemanconcea), plantium plastium genarium (e.g. Phymatorionium (e.g. Phymat fusarium culmorum, FCWP1. Also included is a fusion protein between the 

Sequence 116 AA;

Gaps 0 55.3%; Score 42; DB 7; Length 116; 43.8%; Pred. No. 11; ive 6; Mismatches 3; Indels Local Similarity 43.8 Query Match

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1 MEKVQYLTRSAIRRAE 16 

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Job time : 67.2 secs

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Sequence 2, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 181, App
Sequence 24/91, App
Sequence 28362, A
Sequence 752, App
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Sequence 1, Appli
Sequence 4, Appli
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19332, A
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                                                                          October 1, 2004, 12:07:51; Search time 17 Seconds (without alignments) 48.589 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-063-3

US-09-252-063-7

US-09-252-091A-24791

US-09-252-991A-24791

US-09-252-991A-18000

US-09-198-452A-752

US-09-198-452A-752

US-09-198-452A-752

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US-09-198-452A-752

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Gapop 10.0 , Gapext 0.5
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TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
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EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09252063
Patent No. 6538022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEKVQYLTRSAIRRA 15
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                                                                                                                                                                                                                                                                                 -09-252-063-9
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US-09-252-063-2
| Sequence 2, Application US/09252063 | Sequence 2, Application US/09252063 |
| Sequence 2, Application US/09252063 | Sequence 2, Application US/09252063 |
| APPLICANT INFORMATION: | APPLICANT: Valore, Marting APPLICANT: Tenhunen, Jukka | APPLICANT: Yipertula-Ikonen, Marjo | APPLICANT: Yipertula-Ikonen, Marjo | APPLICANT: Yipertula-Ikonen, Marjo | APPLICANT: Yipertula-Ikonen | APPLICANT: Carla | APPLICANT: Carla | APPLICANT: Carla | APPLICANT: Carla | APPLICANT: Carla | APPLICANT: Carla | APPLICANT: Carla | APPLICANT: Carla | APPLICANT: Saivola | Juha | TITLE OF INVENTION: Carla | Carla | APPLICANT: INORDER: US/09/252,063 | CURRENT FILING DATE: 1997-09-24 | EARLIER PILING DATE: 1997-09-24 | EARL
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GENERAL INFORMATION:
APPLICANT: Pollesello, Piero
APPLICANT: Obaska, Martti
APPLICANT: Obaska, Martti
APPLICANT: Videaka, Jukka
APPLICANT: Videaka, Jukka
APPLICANT: Videaka, Jukka
APPLICANT: Videaka, Juha
APPLICANT: Tilpertula-Ikonen, Marjo
APPLICANT: Tilpertula-Ikonen, Marjo
APPLICANT: Tilpertula-Ikonen, Marjo
APPLICANT: Tilpertula-Ikonen, Marjo
APPLICANT: Tilpertula-Ikonen, Marjo
APPLICANT: Tilpertula-Ikonen,
FILE REFERENCE: 1020
TITLE OF INVENTION: Ca-APPRE (Phospholamban Inhibitors)
FILE REFERENCE: 1020-02000
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENTH: 52
TURENT: 52
                                                                             Gaps
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   Length 52;
                                                                         0; Indels
Query Match 93.4%; Score 71; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0;
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; Sequence 3, Application US/09252063
; Patent No. 6538022
                                                                                                                                                  1 MEKVQYLTRSAIRRA 15
                                                                                                                                                                                                        1 MEKVQYLTRSAIRRA 15
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Best Local Similarity 93.35
Matches 14, Conservative
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; ORGANISM: Canis sp.
US-09-252-063-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Sus sp.
US-09-252-063-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y APPLICANT: POllecello, Piero
APPLICANT: Pollecello, Piero
APPLICANT: Pollecello, Marti
APPLICANT: Ovaska, Marti
APPLICANT: Ovaska, Marti
APPLICANT: Videren, Jukka
APPLICANT: Videren, Jukka
APPLICANT: Vilgenttula-Ikonen, Marjo
APPLICANT: Vilgenttula-Ikonen, Marjo
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
TITLE OF INVENTION: Ca-APPase (Phospholamban Inhibitors)
FILE REPERENCE: 1102.025001
CURRENT APPLICATION NUMBER: 08/92-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER PLING DATE: 1999-02-18
EARLIER PLING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
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93.4%; Score 71; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                      Query Match 93.4%; Score 71; DB 4; Length 52; Best Local Similarity 100.0%; Pred. No. 1.6e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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Sequence 15, Application US/09549872B
Sequence 15, Application US/09549872B
Sequence 15, Application US/09549872B
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Begaert, Thickry
ITILE NEFERBACE: D00590/70008 (JRV/RE)
FILE REFERBACE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US 9908670.4
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR PILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-063-6
; Sequence 6. Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus sp.
US-09-252-063-6
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US-09-732-210-181
Query Match
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APPLICANT: Polleeello, Piero
APPLICANT: Polleeello, Piero
APPLICANT: Polleeello, Dukka
APPLICANT: Tenhunen, Jukka
APPLICANT: Tenhunen, Unkka
APPLICANT: Yliperttula-Ikonen, Marjo
APPLICANT: Tigmann, Carlore, Timo
APPLICANT: Tigmann, Carlore, Timo
APPLICANT: Kaivola, Juha
APPLICANT: Kaivola, Juha
APPLICANT: Kaivola, Juha
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Ca-Arpase (Phospholamban Inhibitore)
TITLE OF INVENTION: Ca-Arpase (Phospholamban Inhibitore)
TITLE OF INVENTION: Ca-Arpase (Phospholamban Inhibitore)
TITLE OF INVENTION: Ca-Arpase (Phospholamban Inhibitore)
TITLE OF INVENTION NUMBER: US/09/252,063
CURRENT FILING DAFE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
SEQ ID NO 7
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                                                                         0; Gaps
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                     Query Match 89.5%; Score 68; DB 4; Length 52; Best Local Similarity 93.3%; Pred. No. 6.1e-06; Matches 14; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zwaal, Richard
APPLICANT: Zwaal, Richard
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierery
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
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Patent No. 6538022
                                                                                                                            1 MEKVOYLTRSAIRRA 15
                                                                                                                                                    1 MEKVQYLTRSAIRRA 15
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; ORGANISM: Gallus sp.
US-09-252-063-7
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                                                                                                                                                                                                                                                                           -09-549-872B-14
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US-09-252-063-7
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LENGTH: 52
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US-09-252-991A-24791

J Sequence 24791, Application US/09252991A

Sequence 24791, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANTION:

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER: OF SEQ ID NOS: 33142

LENGTH: 765
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APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Attanck, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Maturanck, Cindy A.
APPLICANT: Way, Younde S.
TITLE OF INVENTION Anti-fungal Proteins and Methods for Their Use
FILE REPRENCE: 38-21(15.036)B
CURRENT APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR PILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 181
LENGTH: 116
                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.3%; Score 42; DB 4; Length 116; Best Local Similarity 43.8%; Pred. No. 1.3; Matches 7; Conservative 6; Mismatches 3; Indels
88.2%; Score 67; DB 4; Length 52; 86.7%; Pred. No. 9.4e-06; Live 2; Mismatches 0; Indels
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; Patent No. 6573361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Streptomyces coelicolor
US-09-732-210-181
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                                                                                                           1 MEKVQYLTRSAIRRA 15
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                                                                                                                                                              1 MEKVOYITRSALRRA 15
                               Best Local Similarity 86.73
Matches 13; Conservative
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Best Local Similarity 53.3³
Matches 8, Conservative
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Gaps

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Sequence 752, Application US/09198452A

Sequence 752, Application US/09198452A

GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 910-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 752

LENGTH: 235
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: ANCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AREQUENCES FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AREQUENCES: 107196.136

CURRENT FILE REPERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1900
                     51.3%; Score 39; DB 4; Length 210; 53.3%; Fred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 4; Length 235;
Pred. No. 17;
2; Mismatches 4; Indels
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Best Local Similarity 50.0%; Pred. No. 79;
Matches 7; Conservative 4; Mismatches 3; Indels
                                                                      4; Indels
                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-18000
; Sequence 18000, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 18, Application US/08588983 ; Patent No. 5854067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-752
                                                                                                                                                                  180 EAHQYLSREAMKRRE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                   2 EKVQYLTRSAIRRAE 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEKVQYLTRSAIRR 14
Ouery Match
Best Local Similarity 53.5%
Each Local Similarity 53.5%
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                         RESULT 15
US-09-198-452A-752
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US-08-588-983-18
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Sequence 28362, Application US/09252991A
Patent NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILES REPRENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28362
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.0%; Score 39.5; DB 2; Length 835; 66.7%; Pred. No. 36; 1; Indels tive 3; Mismatches 1; Indels
                                          US-08-968-751-4
; Sequence 4, Application US/08968751
; Parent No. 15948643
; GENERAL INFORMATION:
; APPLICANT: Rubinfeld, Bonnee
; APPLICANT: Polakis, Paul G.
; APPLICANT: Ligenfelter, Carol
APPLICANT: Wong, Terilyn T.
; TITLE OF INVENTION: MODULATORS OF BRCA1 ACTIVITY
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILING JAILS.

CLASSIFICATION: 435
ATTORNEY/AGRYT IRFORMATION:
NAME: Glotta, Gregory
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX1024 GG
TELECOMMUNICATION INFORMATION:
TELEPROSE: (510) 262-9758
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 835 amino acids
                                                                                                                                                                                                                                                                                                              ADDRESSEE: ONYX Pharmaceuticals, Inc. STREET: 3031 Research Drive CITY: Richmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28362
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712 EEVTHLTRS-LRRAE 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%
Matches 10; Conservative
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US-09-252-991A-28362
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                     RESULT 13
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US-09-489-039A-11071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,976
FILING DATE: CONCURRENTLY herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FUSSEY, Shelley P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-588-976-18

Sequence 18, Application US/08588976

Patent No. 589170:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTION: Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,983
FILING DATE: Concurrently herewith CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
APPLICANT: Christopher B. Newgard, et al.
TILLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: for Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fussey, Shelley P.M.
REGISTRATION NUNBER: 39,458
REPERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUNICATION INFORMATION:
                                                                                                                              ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          638 ODVVÝLLŘEAÍŘŘRO 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EKVQYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 924 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
1 TOPOLOGY: linear
US-08-588-983-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 53.3.
Best Local 8; Conservative
                                                                                                                                                                                                                COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: TX
COUNTRY: US
ZIP: 77210
                                                                                                                                                                           CITY:
STATE:
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GENERAL INCRMATION:

APPLICANT: GATY BLECON et. al

APPLICANT: GATY BLECON et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREDATOR ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREDATOR SOURCES

TITLE OF INVENTION: DATE: 2709-2004001

CURRENT FILING DATE: 2709-2004001

CURRENT FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 7119

LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MS-09-489-039A-11071
Sequence 11071, Application US/09489039A
Sequence 11071, Application US/09489039A
Sequence 11071, Application US/09489039A
FREATH NO. 6610836
FITUE OF INVENTION: WOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: WOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: WOMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
FRIOR REPLICATION NUMBER: US 60/117,747
FRIOR REPLICATION NUMBER: US 60/117,747
FRIOR PRIOR FILING DATE: 1999-01-29
NUMBER 09 SEQ ID NOS: 14342
LENGTH: 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.4%; Score 36; DB 4; Length 98; 58.3%; Pred. No. 15; 2; Indels tive 3; Mismatches 2; Indels
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 7319, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-7319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                            TELEX: n/a
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                638 QDVVYLLREAIRRO 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EKVQYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53,33
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.35
Matches 7, Conservative
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US-08-588-976-18
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Pred. No. 92;
3; Mismatches 4; Indels
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47.4%; Score 36; DB 4; L
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09342647A
Sequence 2, Application US/09342647A
Sequence 10. 658840
SEGNERAL INPORMATION
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hiz, William D.
APPLICANT: Hiz, William D.
APPLICANT: Milliam D.
TITLE OF INVENTION: ACYL-COA Oxidase Homologs
TILE REFERENCE: BB-1175
CURRENT APPLICATION NUMBER: US/09/342,647A
CURRENT FILING DATE: 1999-06-29
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 630
                                                                                                                                                                                                                                                                                                                                                                                                                                  97-7613/LC (WMC) /1
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                      OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,581B
FILING DATE: December 16, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/489,733
APPLICATION NUMBER: 08/489,733
ATTORNEY/AGENT: UND 14, 1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 97-74
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEPAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 MGKVQYLMQCKSAVSSAE 438
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46.2%;
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Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide US-08-993-581B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
  Washington
                        D.C.
: U.S.A.
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US-09-342-647-2
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                                                               20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-342-647-2
                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Sequence 6, Application US/08993581B
Sequence 5, Application US/08993581B
Sequence 7. Sequence 6, Application US/08993581B
Sequence 7. Sequence 7. Sequence 7. Sequence 7. Sequence 7. TITLE OF INVENTION: HYPERTHERMOSTABLE -GALACTOSIDASE GENE, TITLE OF INVENTION: ENZYME ENCODED THEREBY, AND PROCESS FOR PRODUCTION (AS AMENDED OF SEQUENCES): ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                        ö
                        0; Gaps
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GENERAL INFORMATION:

APPLICANT: Atsushi SHIMADA et al.

TITLE OF INVENTION:

WITHER OF INVENTION:

WORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 47.4%; Score 36; DB 1; Length 489; Local Similarity 46.2%; Pred. No. 92; hes 6; Conservative 3; Mismatches 4; Indels
                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
Best Local Similarity 58.3%; Pred. No. 33; Matches 7; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCETWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/489,733
FILING DATE: June 14, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/175,533
FILING DATE: December 30, 1993
ATTORNEY AGENT INFORMATION:
NAME: WAFFEN M. Cheek, Jr.
REGISTATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 469 amino acids TYPE: amino acid STRANDEDNESS: single
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                                                                                                            111 MERVEYLLOSOI 122
                                                                  1 MEKVQYLTRSAI 12
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MOLECULE TYPE: peptide
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COUNTRY: U.S.A.
ZIP: 20005
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Matches
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Search completed: October 1, 2004, 12:21:11
Job time : 18 secs
US-07-642-734C-4
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                                    Sequence 19332, Application US/09252991A

Sequence 19332, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Whenfield et al.
APPLICANT: Marc J. Whenfield et al.
APPLICANT: Marc J. Whenfield et al.
APPLICANT: Marc J. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 19332

LENGTH: 686
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47.4%; Score 36; DB 4; Length 686;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REPERSTORCET NUMBER: 4552.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 amino acids
                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19332
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MOLECULE TYPE: protein
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                 RESULT 24
US-09-252-991A-19332
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US-07-642-734C-4
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47.4%; Score 36; DB 2; Length 3567; 70.0%; Pred. No. 8.5e+02; tive 2; Mismatches 1; Indels
 Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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Gaps

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                   October 1, 2004, 12:18:23 ; Search time 63.4 Seconds (without alignments) 81.211 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1351062 seqs, 321799191 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                              OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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| core distribution. |            | Description | Sequence 13, Appl | Sequence 12, Appl | Sequence 1, Appli | 18               | ω               | H                | 10               | Sequence 2, Appli | 4,              | 'n  | 15,              | Sequence 478, App  | ٦               | 7               | 'n              |  |
|--------------------|------------|-------------|-------------------|-------------------|-------------------|------------------|-----------------|------------------|------------------|-------------------|-----------------|-----|------------------|--------------------|-----------------|-----------------|-----------------|--|
| of the total s     | SUMMARIES  | ΔI          | US-10-705-791-13  | US-10-705-791-12  | US-09-954-571-1   | US-10-705-791-18 | US-10-705-791-8 | US-10-705-791-11 | US-10-705-791-10 | US-09-954-571-2   | US-09-954-571-4 | ,   | US-10-371-101-15 | US-10-408-765A-478 | US-10-705-791-1 | US-10-705-791-2 | US-10-705-791-5 |  |
| analysis           |            | tch DB      | 35 16             | 9                 | 2                 | 79 16            | 9               | 5                | 1 9              |                   | 2 1             | 2   | 2                | 2 1                | 52 16           | 52 16           | 52 16           |  |
| by an              |            | h Length    | 0                 | 0                 | 0                 | 0                | 4.              | 4                | 4                | 4                 | 4               | 4   | 4                | 4                  | 4               | 4               | 4               |  |
|                    | *<br>Query | :           | 100.              | 100.0             | 100.              | 100.             | 93.             | 93               | 93.              | 93.               | 93.             | 93. | 93.              | 93.                | 93.             | 93.             | 93.             |  |
| and is derived     |            | Score       | 76                | 16                | 16                | 16               | 71              | 71               | 71               | 71                | 71              | 71  | 71               | 71                 | 71              | 71              | 71              |  |

| 17, App<br>e 19, App<br>e 14, App<br>e 4, App<br>e 4, App<br>e 3, App<br>e 10177,<br>e 238702,<br>e 46161,<br>e 46161,<br>e 4944, Ap                                                                                                                                                                                                                             | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                         | 2 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 2 1 1760 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| S-10-705-791-17 S-10-705-791-19 S-10-705-791-19 S-10-371-101-14 S-10-705-791-3 S-10-705-791-3 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-6 S-10-705-791-791-791-791-791-791-791-791-791-791 | 5 10 - 36 9 49 9 - 20 3 8 10 - 36 9 49 9 - 20 3 8 10 - 36 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | 20007 BOOM THE BOOM CONTROL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
CURRENT SEPERENCE: 6627-P49925
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
LENGTH: 36
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Sequence 1, Application US/09954571

Sequence 1, Application US/09954571

Publication No. US20020032167A1

GENERAL INFORMATION:

APPLICANT: Chier, Kenneth R

APPLICANT: Ross, John

APPLICANT: Ross, John

APPLICANT: Ross, John

TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER

TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER

CURRENT FILLING DATE: 2001-09-11

PRIOR FILING DATE: 2001-09-11

PRIOR FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.2

SEQ ID NO 1

LENGTH: 52

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| Publication No. US20040121942A1
| GENERAL INFORMATION:
| APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth
| APPLICANT: Dillmann, Wolfgang
| APPLICANT: Dillmann, Wolfgang
| APPLICANT: He, Huaping
| APPLICANT: He, Huaping
| APPLICANT: Hoshijima, Masahiko
| APPLICANT: Soott, Caristopher
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** O'THEN PORMATION: Mutant form of humam protein sequence
US-09-954-571-1
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100.0%; Pred. No. 1.7e-06;
tive 0; Mismatches 0;
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Matches 16; Conservative
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) ORGANISM: Homo sapiens
US-10-705-791-12
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Best Local Similarity
Matches 16; Conserv
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APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Howinisewa, Susanne
APPLICANT: Howining Masahiko
APPLICANT: Hoshifina, Masahiko
APPLICANT: Hoshifina, Masahiko
APPLICANT: Mang, Yibin
APPLICANT: Scott, Christopher
APPLICANT: Short Markus
APPLICANT: Mang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE REFERENCE: 6627-PA9025
CURRENT FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE PATENTIN VERSION 3.2
                                                                                             Sequence 442, App
Sequence 442, App
Sequence 464, App
Sequence 222332,
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Sequence 11067, A
               Sequence 4858, Ap
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Sequence 38, Appl
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      US-09-864-408A-4858
US-10-424-599-152503
US-10-372-876-442
US-10-097-065-442
US-10-112-944-464
US-10-12-944-464
US-10-12-944-464
US-10-424-122A-71415
US-10-282-122A-71415
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US-10-425-114-52269
US-10-156-761-11067
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Publication No. US20040121942A1
GENERAL INFORMATION:
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; Sequence 12. Application US/10705791
; Publication No. US2040121942A1
; GENERAL INFORMATION:
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US-10-705-791-13
               JS-10-705-791-13
               SEQ ID NO 13
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APPLICANT:
APPLICANT:
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APPLICANT: He, Kuaping
APPLICANT: Hoshijma, Masahiko
APPLICANT: Hoshijma, Masahiko
APPLICANT: Hoshijma, Masahiko
APPLICANT: Hoshijma, Masahiko
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Slotterman, Gregg J.
APPLICANT: Slotterman, Gregg J.
APPLICANT: Slotterman, Gregg J.
TITLE OF INVENTION: WETHOO FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: WETHOO FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: WIMBER: US/10/705,791
CURRENT APPLICATION NUMBER: G0/106,718
FRIOR APPLICATION NUMBER: FCT/US99/25692
FRIOR APPLICATION DATE: 1998-11-02
FRIOR APPLICATION NUMBER: FCT/US99/25692
FRIOR APPLICATION NUMBER: FCT/US99/25692
FRIOR APPLICATION NUMBER: PCT/US99/25692
FRIOR APPLICATION OF SEQ ID NOS: 19
SOFTWARE: Parentin version 3.2
SEQ ID NO 10
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                            APPLICANT: Silverman, Gregg J.

TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT PILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR SPLING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VOS: 19
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                        APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Dillmann, Wolfgang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: The Regents of the University of California APPLICANT: Chian, Kenneth APPLICANT: Chilmann, Wolfgang APPLICANT: Minamisawa, Susanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
93.4%; Score 71; DB 16; L
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 10, Application US/10705791; Publication No. US20040121942A1; GENERAL INFORMATION:
                                                                                                                                      APPLICANT: He, Humping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
                                                                                                                   Minamisawa, Susanne
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Best Local Similarity 100.0
Matches 15; Conservative
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US-10-705-791-11
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US-10-705-791-10
GENERAL INFORMATION:
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US-10-705-791-10
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                     APPLICANT: SILVERMAN, GREGG J.

TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REPERRNCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US,10/705,791
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 79
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100.0%; Score 76; DB 16; Length 79;
Best Local Similarity 100.0%; Pred, No. 2.6e-06;
Marches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Regents of the University of California APPLICANT: Chian, Kenneth APPLICANT: Chilmann, Wolfgang APPLICANT: Minamisawa, Susanne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
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US-10-705-791-18
APPLICANT: Wang, Yibin
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US-10-705-791-8
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US-10-705-791-11
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US-10-705-791-8
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APPLICANT: Chien, Kenneth R
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
Ross, John
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFRENCE: 6627-PA0123
FILE REFRENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/05/954,571
CURRENT FILING DATE: 2001-09-11
PRICR APPLICATION NUMBER: 66/231,821
PRICR PILING DATE: 2000-11-09
NUMBER OF SEQ 1D NOS: 5
SOFTWARE: PatentIn version 3.2
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Sequence 15, Application US/10371101
Sequence 15, Application US/10371101
Sequence 15, Application US/10371101
Sequence 15, Application US/10371101
SEGUENCEAL INPORMATION:
APPLICANT: Zwall, Richard
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035.US
CURRENT FILING DATE: 2003-02-21
FRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SECTUMARE: PALENTH VET: 2.00
SEQ ID NO 15
LENTH: S2
LENTH: S2
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LENGTH: 52
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
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ORGANISM: Homo sapiens
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Matches 15; Conserva
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-408-765A-478
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Sequence 4, Application US/09954571

Publication No. US20020032167A1

GENERAL INPORMATION:

APPLICANT: Chien, Kenneth R

APPLICANT: Hoshijima, Masahiko

APPLICANT: Ross, John

APPLICANT: Ikeda, Yasuhiro

TITLE OF INVENITON: HIGH EFFICIENCY CARDIAC GENE TRANSFER

FILE REFERENCE: 6627-PA0123

CURRENT APPLICATION NUMBER: US/09/954,571

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: 60/231,821

PRIOR FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                GAPPLICANT: Chien, Kenneth R
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
TELS BORES, JOHN
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REPRENCE: 6627-PA0123
FILER REPRENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION WIMBER: 60/231,821
PRIOR FILING DATE: 200-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VETSION 3.2
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93.4%; Score 71; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                     US-09-954-571-2; Sequence 2, Application US/09954571; Publication No. US20020032167A1; GENERAL INFORMATION:
                                           1 MEKVQYLTRSAIRRA 15
1 MEKVOYLTRSAIRRA 15
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ORGANISM: Homo sapiens
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LENGTH: 52
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LENGTH: 52
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; Sequence 5, Application US/09954571 ; Publication No. US20020032167A1

RESULT 10 US-09-954-571-5

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APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: Scott, Christopher
APPLICANT: Silverman, Gregor
APPLICANT: Silverman, Gregor
APPLICANT: Silverman, Gregor
APPLICANT: Silverman, Gregor
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: Of/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOTUMARE: Patentin version 3.2
SEQ ID NO
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TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
FILMS APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: 60/106,718
PRIOR PILING DATE: 1999-11-02
PRIOR PADLICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SSO THARKE: PATENTIN VERSION 3.2
SEQ ID NO 5
LENGTH: 52
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Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
93.4%; Score 71; DB 16; I
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0;
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Pred. No. 1.4e-05;
0; Mismatches 0;
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1 Similarity 100.0%; P1
15; Conservative 0;
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T: Hoshijima, Masahiko
T: Meyer, Markus
T: Scott, Christopher
T: Wang, Yibin
                                                                                     Minamisawa, Susanne
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                                                 Dillmann, Wolfgang
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US-10-705-791-5
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INLIEITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: Us/10/705,791
CURRENT PILING DATE: 2003-11.10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR PILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version,3.2
SEQ ID NO 1
LENGTH: 52
TWIST SILVER SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND S
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          APPLICANT: GLOCK, CERTING APPLICANT: GLOCK, CALVEN APPLICANT: Glon, Gary M.
APPLICANT: Glon, Gary M.
APPLICANT: Glon, Gary M.
ITILE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DEBMIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFRENCE: 66008.465
CURRENT PALICALTON NUMBER: US/10/408,765A
CURRENT FLING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEPTWARE: PASTESEQ for Windows Version 4.0
SEQ ID NO 478
LENGTH: 52
TYPE: PRT
CORGANISM: Home sapiens
US-10-408-765A-478
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Publication No. US20040121942A1
GENERAL INFORMATION:
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Publication No. US20040121942A1
GENERAL INFORMATION:
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Hoshljima, Masahiko
Meyer, Markus
Scott, Christopher
Wang, Yibin
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Dillmann, Wolfgang
Minamisawa, Susanne
Gibson, Bradford W. Taylor, Steven W.
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Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-10-705-791-1
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US-10-705-791-2
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APPLICANT:
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Publication No. US2020032167A1

Publication No. US2020032167A1

GENERAL INFORMATION:

APPLICANT: Chien, Kenneth R

APPLICANT: Hoshijima, Masshiko

APPLICANT: Ross, John

TITLE OF INVENTION: HIGH EPPLICIENCY CARDIAC GENE TRANSFER

FILE REPRENSUE: 6627-PA0123

FILE REPRENSUE: 6627-PA0123

CURRENT APPLICATION NUMBER: US/09/954,571

PRIOR APPLICATION NUMBER: 06/231,821

PRIOR PILING DATE: 2001-09-11

PRIOR FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 5

SOFUTANTE: PATENTIN VERSION 3.2

SEQ ID NO 3

LENGTH: 52
                                                                                                                                       Length 79;
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                                                                                                                                  93.4%; Score 71; DB 16; I
100.0%; Pred. No. 2.2e-05;
tive 0; Mismatches 0;
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Publication No. US2033014995A1

GENERAL INFORMATION:

APPLICANT: Zwaal, Richard

APPLICANT: Groenen, Jose

APPLICANT: Bogaert, Thierry

TITLE OF INVENTION: COMPOUND SCREENING METHODS

FILE REFRENCE: D00590.70035.US

CURRENT APPLICATION NUMBER: US/10/371,101

CURRENT APPLICATION NUMBER: US 60/129,596

FRIOR APPLICATION NUMBER: US 60/129,596

FRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-06-15

FRIOR FILING DATE: 1999-06-15

FRIOR FILING DATE: 1999-06-15

FRIOR FILING DATE: 1999-06-01

FRIOR FILING DATE: 1999-06-01

FRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 4

LENGTH: 52
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US-09-954-571-3
; ORGANISM: Escherichia coli
US-10-705-791-19
                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 93.34
Matches 14; Conservative
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APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Chien, Kenneth
APPLICANT: Dillaman, Wolfgang
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: Hoshilina, Masahiko
APPLICANT: Hoshilina, Masahiko
APPLICANT: Mang, Yibin
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: 6010-100
TITLE OF INVENTION: OF CARDIAC DISBASE
TITLE OF INVENTION: OF CARDIAC DISBASE
CURRENT FILING DATE: 2003-11-10
FRIOR PRICATION NUMBER: 60/106,718
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1999-11-02
FRIOR FILING DATE: 1990-11-02
FRIOR FILING DATE: 1990-11-02
FRIOR FILING DATE: 1990-11-02
FRIOR FILING DATE: 1990-11-02
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93.4%; Score 71; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Chien, Kenneth APPLICANT: Dillmann, Wolfgang APPLICANT: Minamisawa, Susanne APPLICANT: He, Huaping APPLICANT: He, Huaping APPLICANT: Heshijima, Masahiko APPLICANT: Scott, Christopher APPLICANT: Scott, Christopher APPLICANT: Wang, Yibin
                                                                                                                                                                                                                  Sequence 17, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
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; ORGANISM: Escherichia coli
US-10-705-791-17
                                                                                                                                  RESULT 16
US-10-705-791-17
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LENGTH: 79
TYPE: PRT
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APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Wolfgang
APPLICANT: Minamisawa, Susanne
APPLICANT: He Huaping
APPLICANT: He Huaping
APPLICANT: Goot, Christopher
APPLICANT: Scott, Christopher
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81.6%; Score 62; DB 16;
Best Local Similarity 86.7%; Pred. No. 0.00064;
Matches 13; Conservative 1; Mismatches 1;
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Publication No. USZ0030119018A1
SPELICANT: OMURA, SATOSHI
APPLICANT: OMURA, SATOSHI
APPLICANT: SHEMA, TARDO,
APPLICANT: HERDA, UNN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHEMA, TADAYOSHI
APPLICANT: ASHRAY, TADAYOSHI
APPLICANT: APTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 52
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US-10-705-791-6
                                                                                                                              TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-3
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US-10-156-761-10177
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US-10-705-791-6
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APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: Meyer, Markus
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Silverman, Gregal
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT PILING DATE: 2003-11-10
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
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TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REPERENCE: 6627-PA$025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR SELING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
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Best Local Similarity 93.3%; Pred. No. 5e-05;
Matches 14; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Chien, Wenneth APPLICANT: Dilmann, Wolfgang APPLICANT: Minamisawa, Susanne APPLICANT: He, Huaping APPLICANT: He, Huaping APPLICANT: Meyer, Markus APPLICANT: Scott, Christopher APPLICANT: Wang, Yibin
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                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10705791 Publication No. US20040121942A1 GENERAL INFORMATION:
                                                                                                        1 MEKVOYLTRSAIRRA 15
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US-10-705-791-4
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US-10-705-791-4
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US-10-705-791-3
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LENGTH: 52
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53.9%; Score 41; DB 12; Length 68; 71.4%; Pred. No. 6.5; tive 0; Mismatches 4; Indels
); ORGANISM: Zea mays:
; FEATURE:
; OTHER INFORMATION: Clone ID: 701164165_FLI.pep
US-10-425-114-46161
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Best Local Similarity
Matches 10; Conserv
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: About K
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
EEQ ID NO 238702
LENGTH: 44
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Schou, Yihua
APPLICANT: Schou, Steven K
APPLICANT: Schou, Steven K
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei I
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 46161
LENGTH: 68
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_57573C.1.pep
US-10-424-599-238702
                   PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FLING DATE: 2001-05-30 PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02 NUMBER OF SEQ ID NOS: 15109 LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 238702, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 46161, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION;
                                                                                                                                                                                                  TYPE: PRT;
GRGANISM: Streptomyces avermitilis
US-10-156-761-10177
     CURRENT FILING DATE: '2002-05-29
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81 VEKIELVTRGDVRRAK 96
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Best Local Similarity 46.2
Matches 6; Conservative
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25 LEKIEYITRERIK 37
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US-10-424-599-238702
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US-10-425-114-46161
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 100 summaries
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C, Accession: A49057

R, Ganim, J. R.; Luo, W.; Ponniah, S.; Grupp, I.; Kim, H.W.; Ferguson, D.G.; Kadambi, V.; N. C, Accession: A49057

R, Ganim, J. R.; Luo, W.; Ponniah, S.; Grupp, I.; Kim, H.W.; Ferguson, D.G.; Kadambi, V.; N. C, T.; Res. T.; 1021-1030, 1992

A, Title: Mouse phospholamban gene expression during development in vivo and in vitro. A; Reference number: A49057; MUID:93008802; PMID:1394867

A, Accession: A49057

A, Accession: A49057

A, Residues: 1-52 -GANN

A; Residues: 1-52 -GANN

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A; Residues: 1-52 -GANN

C, Comment: Phospholamban is expressed in cardiac muscle, succession and comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm

C, Comment: Phospholamban is the major phosphorylated protein in cardiac muscle relaxation in C; Superfamily: phospholamban is the major phosphorylated protein in cardiac muscle relaxation in C; Superfamily: phospholamban

C, Reywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tri
F; 11-52/Domain: transmembrane #status predicted F; 11-Fill of site: acetylated amino end (Met) #status predicted
F; 16/Phinding site: phosphate (Ger) (covalent) (by calmodulin-dependent kinase) #status predicter
F; 17/Phinding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase)
                                A. Structus: preliminary; translated from GB/EMBL/DDBJ
A. Molecule type: mRNA
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C;Date: 19-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.4%; Score 71; DB 1; Length 52; 100.0%; Pred. No. 4.6e-06; tive 0; Mismatches 0; Indels
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A; Accession: I51840
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R;Ftjii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
J. Biol. Chem. 266, 11669-11675, 1991
A? Etters Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assi A;Accession: A40424; MUID:91268032; PMID:1828805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Molecule type: mRNA
A;Residues: 1-52 cFUD.
A;Cross-references: GB:W63603; NID:g189942; PIDN:AAA60083.1; PID:g189943
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, art
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplae
C;Comment: Phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is
C;Comment: Helical transmembrane domains of five chains are thought to aggregate in the
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A. Molecule type: mENA
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A. Molecule type: MENA
A. Cross-references: EMEL:X71068; NID:9313809; PIDN:CAA50394.1; PID:9313810
B. Johns, D. C.; Feldman, A.M.
B. Johns, D. C.; Feldman, A.M.
B. Johns, D. C.; Feldman, A.M.
A. A. Cross-reference on English of a highly conserved region at the 5' flank of the phospholamba
A. Reference number: 152270
A. A. A. Cross-reference on Muld: 93075183; PMID:1445334
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-52 JOHN
A. Molecule type: DNA
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F;31-52/Domain: transmembrane #status predicted <TMM>
F;1/Modified site: acetylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
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Cibate 05-Mar-1994 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
Cibatession: S37638, 152270; 164795; 151840
Rishanahan, C.M.; Weissberg, P.L.; Metcalfe, J.C.
Circ. Rss. 73, 193-204, 1993
A;Title: Isolation of gene markers of differentiated and proliferating vascular smooth A;Reference number: S37637; MUID:93284726; PMID:8508530
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                                                                                                                                                                                                                                                                                                                                       .Species: Homo sapiens (man)
.Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
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Pred. No. 4.6e-06; 
0; Mismatches 0; Indels
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100.0%; Pred. No. ...
... 0; Mismatches
      AL IGNMENTS
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A.Cross-references: GDB:128300; OMIM:172405
A.Map position: 6922.1-6922.1
C.Superfamily: phospholamban
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A; Residues: 1-52 <HWA1>
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phospholamban - rabbit character rabbit)
C;Species Orycolagus cuniculus (domestic rabbit)
C;Species 10 - Vocolagus cuniculus (domestic rabbit)
C;Species 128-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Accession: B40424, 800249
B;Nujii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
J; Biol. Chem. 266, 11669-11675, 1991
A;Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assig A;Accession: B40424
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-52 FUU>
A;Cross-references: GB:M63601; NID:g165636; PIDN:AAA31445.1; PID:g165639
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Score 71; DB 1; Length 52;
Pred. No. 4.6e-06;
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                     100.0%; Pred. w..
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A;Accession: 146227
A;Betatus: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: 1.52 <urs.
A;Residues: 1.52 <urs.
A;Residues: 1.52 <urs.
A;Crosw-references: GB M3593; NID:g164045; PIDN:AAC41618.1; PID:g164046
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch SkWeletal muscle sarcoplasm
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
C;Comment: Phospholamban is the major phosphorylated and the rate of muscle relaxation is c;Reywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
C;Reywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F;13-52/Domain: transmembrane #status predicted <ur>F:14.52/Domain: cactylated amino end (Met) #status experimental
F;16/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status experim F;16/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status experim
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R;Verboomen, H.; Wuytack, F.; Eggermont, J.A.; de Jaegere, S.; Missiaen, L.; Raeymaekers, Blochem, J. 262, 335-356, 1989
A;Title: CDNA cloning and sequencing of phospholamban from pig stomach smooth muscle. A;Reference number: S05540; MUID:90056437; PMID:2530978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Cross-references: EMBL:X15075, NID:92055, PIDN:CAA33171.1, PID:92056
C.Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
C.Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasme, after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation in
C.Superfamily: phospholamban
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C.Species: Sus scrofa domestica (domestic pig)
C.Date: 21-Nov-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 06-Mar-1992 #sequence revision 27-Jun-1994 #text_change 18-Jun-1999
C;Accession: A39535; B39535; Ā44531
R;Toyofuku, T.; Zak, R.
J. Biol. Chem. 266, 5375-5383, 1991
A;Title: Characterization of cDNA and genomic sequences encoding a chicken pareference number: A39535; MUID:9110195; PMID:1825996
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Pred. No. 1.68-05;
Pred. Trinhes 0; Indels
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A;Molecule type: mRNA
A;Residues: 1-17, L'. 19-52 <TOY>
A;Cross-references: GB:M59039; NID:g212575; PIDN:AAA62738.1;
A;Note: the authors translated the codon CTT for residue 18 a
A;Accession: B39535
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Best Local Similarity
Matches 14; Conserv
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Matches 14; Conser
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A; Residues: 1-52 <VER>
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        FIRES Lett. 227, 1988

A,Title: Rabbit cardiac and slow-twitch muscle express the same phospholamban gene.

A,Reference number: 800249; MUID:8811222; PMID:2962883

A,Recession: 800249; MUID:8811222; PMID:2962883

A,Recession: 800249; MUID:88112222; PMID:2962883

A,Steatus: not compared with conceptual translation

A,Accession: S00249

A,Steatus: not compared with conceptual translation

A,Residues: 1-52 < rCUS

A,Cross-references: GB:Y00761; NID:91661; PIDN:CAA68730.1; PID:91662

A,Cross-references: GB:Y00761; NID:91661; PIDN:CAA68730.1; PID:91662

C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and c; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplase; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is c; Genetics:

A,Note: che single intron is upstream of the coding region

C; Superfamily: phospholamban

C; Superfamily: phospholamban

C; Superfamily: phospholamban

C; Superfamily: prospholamban

C; Superfamily: cransmembrane #status predicted ATMN

F;1/Modified site: acetylated amino end (Met) #status predicted

F;11-52/Domain: transmembrane #status (Ser) (covalent) (by cAMP-dependent kinase) #status predict

F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase)
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Pred. No. 4.6e-06;
0; Mismatches 0; Indels
J.; Tada, M.; MacLennan, D.H.
5, 1988
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100.0%; Fit
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Matches 15; Conserv
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Gaps

0

4; Indels

Length 121

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C,Accession: H83370
C,Accession: H83370
R,Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bristover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A,Title. Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                       A;Accession: B70187
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule.type: DNA
A;Residues: 1-121 <KLE>
A;Cross-trences: GB:AE001170; GB:AE000783; NID:g2688623; PIDN:AAC67044.1; PID:g2688625;
A;Experimental source: strain B31
C;Superfamily: Escherichia coli ribosomal protein L19
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hydrogenes: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
A; Reference number: A70100; MUID:98065943; PMID:9403685
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53.9%; Score 41; DB 2;
Best Local Similarity 50.0%; Pred. No. 3.7;
Matches 8; Conservative 4; Mismatches
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Best Local Similarity 46.7%;
Matches 7; Conservative '
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154 EQVRWLDREELRRAE 168
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Best Local Similarity 53.3
Matches 8, Conservative
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                    A;Residues: 1-52 <TC2.
A;Crost-references: GB:MS9038
A;Crost-references: GB:MS9038
A;Octe: the sequence of residues 33-52 and the corresponding nucleotide sequence are not submitted to GenBank, April 1991
A;Accession: A44531
A;Accession: A44531
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
S.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Gand, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
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Cipate: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
Cipacession: T34780
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
B;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A;Reference number: Z21557
A;Accession: T34780
A;Reference number: Z21557
A;Actus: T36410
A;Actus: preliminary; translated from GB/EMBL/DDBU
A;Residues: 1-116 -kWTN
A;Residues: 1-116 -kWTN
A;Residues: 1-116 -kWTN
A;Residues: BMA:AL023797; PIDN:CAA19387.1; GSPDB:GN00070; SCOEDB:SC2E1.12
A;Experimental source: strain A3(2)
Cigenetics: Coedelics:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>;</del>
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Species: Streptomyces coelicolor
Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
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Pred. No. 2.5e-05;
2; Mismatches 0; Indels
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Matches 7; Conserv
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C.Accession: S53487
R.Matters, G.L.; Beale, S.I.
Balle, D.J.; Beale, S.I.
Plant Mol. Biol. 27, 607-617, 1995
A.Title: Structure and expression of the Chlamydomonas reinhardtii alad gene encoding the A.Reference number: S53487; MUID:95201253; PMID:7894023
A.Accession: S53487
A;Cross-references: GB;AE004646; GB:AE004091; NID:g9948213; PIDN:AAG05583.1; GSPDB:GN001: A;Experimental source: strain PAO1
C;Genetics:
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N.Alternate names: delta-aminolevulinic acid dehydratase
C.Species: Chlamydomonas reinhardtii
C.Species: Chlamydomonas reinhardtii
C.Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
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A.Residues: 1-390 cMAT>
A.Cross-references: EMBL:U19876, NID:g642578; PIDN:AAA79515.1; PID:g642579
C.Superfamily: porphobilinogen synthase
C.Keywords: carbon-oxygen lyase; hydro-lyase
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Pred. No. 19;
4; Mismatches 4; Indels
                                                                                                                                                                                                      Length 417;
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                                                                                                                                                                                                   Score 41; DB 2;
Pred. No. 13;
4; Mismatches
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Indels

Length 1027;

2;

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mitotic spindle associated protein, MAP126 - human G'Species: Home sapiens (man)
C'Species: Home sapiens (man)
C'Species: Home sapiens (man)
C'Date: O'IPEb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C'Accession: 407765
R'Chang, M.S.; Huang, C.J.; Chen, M.L.; Chen, S.T.; Fan, C.C.; Chu, J.M.; Lin, W.C.; Yang Alficher. Biophys. Rec. Commun. 287, 116-121, 2001
A;Title: Cloning and characterization of hMAP126, a new member of mitotic spindle-associal A;Contents: Testis
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Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Jun-2003
Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Jun-2003
Ristover, C. K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradaman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
Ailtle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathos A. Reference number: A82950; MUID:20437337; PMID:10984043
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A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1120 <CHA>
A;Cross-references: GB:AF345347
C;Comment: This protein, as a nuclear protein and a new member of kinesin family, which and dynamic regulation of mitotic spindles and may provide an outward force to push the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aliphatic amidase regulator PA3363 [imported] - Pseudomonas aeruginosa (strain PAO1)
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53.3%; Pred. No. 14;
tive 3; Mismatches 4; Indels
                   A;Cross-references: EMBL:AL137585
A;EXPERIMENTAL SOURCE: adult Lestis; clone DKFZp434H1210
C;Genetics:
A;Note: DKFZp434H1210.1
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                                                                                                                                                                                                        52.0%; Score 39.5; D 66.7%; Pred. No. 65; ive 3; Mismatches
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904 EEVTHLTRS-LRRAE 917
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166 EAHQYLSREAMKRRE 180
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Matches 8; Conservative
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Best Local Similarity
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Best Local Similarity
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A;Map position: 17q11-12
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A;Molecule type: DNA
A;Residues: 1-196 <STO>
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                                                                                                                                                                     A;Residues: 1-1108 <KAW>
A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29695.1; PID:d1030638; PID:g32570
A;Cross-rimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by Genbank A;Gene: PH0606
                                                                                                                                                                                                                                                                                                                                                                 M.; Ohfuku, Y.; Funahabli, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Yamanoto, S.; Sekil DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic & A;Accession: E71104
A;Accession: E71104
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-1108 «KAW»
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Jeo.oct-1999 #sequence_revision 29-Oct-1999
C;Accession: T34542
S;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
sibmitted to the Protein Sequence Database, October 1999
A;Reference number: Z21541
A;Reterence number: Z215
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hypothetical protein DKFZp434H1210.1 - human (fragment)
(Species: Indom sapiens (man)
(Species: John Sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
(Spacession: Ty6296
Rybuesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, January 2000
A; Reference number: Z23035
A; Accession: Ty6296
A; Reference protein Ty6296
A; Reference protein Ty6296
A; Reference protein Ty6296
A; Residues: 1-1027 < AAA>
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Score 38; DB Pred. No. 25; 2; Mismatches

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A; Residues: 1-224 -ARNA
A; Residues: 1-224 -ARNA
A; Cross-references: GB:AE001652; GB:AE001363; NID:g4376997; PIDN:AAD18847.1; PID:g437701)
A; Bxperimental source: strain CWL029
B; Read, T.D.; Erunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Mucleic Acids Ree. 20; 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conserved hypothetical protein CP003B [imported] - Chlamydophila pneumoniae (strains CWLK) N.Alternate names: ct68 hypothetical protein
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Accession: D72046; B81620
R;Kalman, S; Mitchell; W; Marathe, R; Lammel, C; Fan, J; Olinger, L; Grimwood, J;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:1019238B
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-224 <REA>
A,Cross-references: GB:AE002167; GB:AE002161; NID:g7188971; PIDN:AAF37933.1; PID:g7188976
A,Experimental source: strain AR39, HL cells
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Crees: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Accession: A86579
S:Ashirab, M.; Hirakawa, H.; Kindoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ish Nacleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Accession: A86579
A;Accession: A86579
A;Accession: Preliminary
A;Accession: A86579
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A;Accession: A86579
A;Accession: A86491; MUD:20330349; MUD:200142
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A; Experimental source: serotype D, strain UM-3/Cx
                                                                                                                              50.08;
                                                                                                                                                                                                                                                                                                                         188 KVOYAVORATORAE 201
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                                                                                                                                                                                                                                                             3 KVQYLTRSAIRRAE 16
                                                                                           Query Match
Best Local Similarity 57.11
Best Local 8; Conservative
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                            C;Genetics:
A;Gene: CT668
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                                                                                                                                                                                                                                                      R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83850; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PAB0334 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: B75167
R;anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
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A.Experimental source: strain Orsay
C.Genetics:
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                                                                                                                       transcription regulator BH0839 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                       C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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A;Status: preliminary
A;Molecule type: DNA
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                                                           RESULT 17
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50.0%; Score 38; DB 2; Length 224;
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C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Dates: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: 155449
S;McCright, B.; Virshup, D.M.
J. Biol. Chem. 270, 26123-26128, 1995
A;Title: Identification of a new family of protein phosphatase 2A regulatory subunits.
A;Reference number: 155449; MUID:96064678; PMID:7592815
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;Cross-references: EMBL:J03918; NID:g1435186; PIDN:AAB04031.1; PID:g172570
                                                                                                                                                                                                                                                                                                                              ô
                                                         A;Residues: 1-462 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06877.1; PID:g16505525; GSPDB:GN00176
C;Genetics:
A;Gene: STY4756
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NyAlternate names: protein YD9489.05c; protein YDR170c
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence revision 23-Aug-1996 #text_change 21-Jul-2000
C;Accession: S49764; S50916; A31068; A28784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Cross-references: GB:L42373; NID:g1000887; PIDN:AAC37601.1; PID:g1000888
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A,Residues: 1-486 <RES>
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Pred. No. 53;
4; Mismatches
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Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 4; Mismatches
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A;Map position: 1q41-1q41
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294 DKVTWMTREASRRGD 308
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19 EKVDGFTRKSVRKAQ 33
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46.7%; Pred. No. 47;
live 4; Mismatches
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2; Mismatches
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57.1%;
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R;Achstetter, T.; Franzusoff, A.; Field, C.; Schekman, R. submitted to the Protein Sequence Database, August 1988
A;Reference number: A34619
A;Recession: A28784
A;Molecule type: DNA
A;Residues: 1-187, 'S',189-398,'LL',399,'C',403-1030,'PAICF',1031,'L',1038-2009 cACH2>
C;Genetics:
A;Genes: SGD:SBC7
A;Genes: SGD:S0002577; MIPS:YDR170c
A;Morp position: 4R
C;Keywords: transmembrane #status predicted <TML>
F;782-598/Domain: transmembrane #status predicted <TML>
F;782-744/Domain: transmembrane #status predicted <TM3>
F;1817-1833/Domain: transmembrane #status predicted <TM3>
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Mortishire-Smith R.J., Pitzenberger S.M., Burke C.J., Middaugh C.R.,
Garsky V.M., Johnson R.G.;
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Solution structure of the cytoplasmic domain of phospholamban: phosphorylation leads to a local perturbation in secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99222499; PubMed=10198197; McTiernan C.F., Frye C.S., Lemster B.H., Kinder B.A., Ogletree-Hughes M.L., Moravec C.S., Feldman A.M.; "The human phospholamban gene: structure and expression."; J. Mol. Cell. Cardiol. 31:679-692(1999).
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                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB)
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                     PRT;
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MEDLINE=98170970; PubMed=9512019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 34:7603-7613(1995).
                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D-STRUCTURE MODELING.
                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                  NCBI_TaxID=9606;
                   PPLA HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structure
                                    P26678
PPLA_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
PHOSPHORYLATION (BY CAMK) (BY
SIMILARITY).
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Herzyk P., Hubbard R.E.; Using angelia model of the Uraing experimental information to produce a model of the language transmembrane domain of the ion channel phospholamban."; Biophys. J. 74:1203-1214(1998).

-!- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.

-!- SUBUNIT: Homopentamer.
                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: Membrane.
-i- TISSUE SPECIFICITY: Heart.
-i- PTM: Phosphorylated in response to beta-adrenergic stimulation.
-i- PTM: Phosphorylated to the phospholamban family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat), and Oryotolagus cuniculus (Rabbit).
Oryotolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090, 10116, 9986;
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Transmembrane; Phosphorylation; Aceylation; 3D-structure.
Transmembrane; Phosphorylation; CyroplasMic (POTENTIAL).
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Pred. No. 1.3e-06;
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52 AA, 6108 MW, 0766304A76A854D3 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. 1.3
ive 0; Mismatches
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EMBL; M60411; AAA60109.1; -.
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PDB; IKSN; I4-NOV-01.
PDB; IKCH; 28-NOV-01.
PDB; IPLN; 29-DEC-99.
PDB; IPLP; 31-UL-95.
PDB; IPSL; 03-UN-95.
Genew; HGNC:9080; PIN.
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P20006;
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                    Pujii J., Lytton J., Tada M., Maclennan D.H.; "Rabbit cardiac and slow-twitch muscle express the same phospholamban
                                                         Fujii J., Zarain-Herzberg A., Willard H.F., Tada M., Maclennan D.H., "Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6."; J. Biol. Chem. 266:11669-11675(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93075183; PubMed=1445334;
Johns D.C., Feldman A.M.;
Jachtification of a highly conserved region at the 5' flank of the
phospholamban gene.";
Biochem. Biophys. Res. Commun. 188:927-933(1992).
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MEDLINE=92008802; PubMed=1394867;
Ganim J.R., Luo W., Ponniah S., Grupp I., Kim H.W., Perguson D.G.,
Kadambi V., Neumann J.C., Doetschman T., Kranias B.G.;
"Mouse phospholamban gene expression during development in vivo and
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-!- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.

-!- SUBGNIT: Homopentamer.

-!- TISSUE SPECIFICITY: Heart.

-!- TISSUE SPECIFICITY: Heart.

-!- TISSUE SPECIFICITY: Heart.

-!- TISSUE SPECIFICITY: Heart.

-!- SIMILARITY: Belongs to the phospholamban family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93284726; PubMed=8508530; Shanahan C.M., Weissberg P.L., Metcalfe J.C.; Shanahan C.M., weissberg P.L., Metcalfe J.C.; Isolation of gene markers of differentiated and proliferating vascular smooth muscle cells."; Circ. Res. 73:193-204(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning phospholamban cDNA from rat aortic smooth muscle."; Adv. Exp. Med. Biol. 304:387-395(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SPECIES=8226(SUB-Aortic smooth muscle, MEDLINE=92266543; PubMed=1725098; Hwang K.S., Nadal-Ginard B.;
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EMEL, M63601, AAA1445.1, -...
EMEL, M63601, AAA1445.1, -...
EMEL, L03382, AAA11849.1, -...
EMEL, L03382, AAA11849.1, -...
EMEL, S95849, AAN86727.1, -...
EMEL, X71068, CAAS0394.1; -...
SPECIES=Rabbit;
MEDLINE=91268032; Pubmed=1828805;
                                                                                                                                                                                                                                                            SPECIES=Rabbit;
MEDLINE=88112222; PubMed=2962883;
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 227:51-55(1988).
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PIR; B40424; B40424.
PIR; S37638; S37638.
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A HSSP; P26678; 1PLP.

R MGD; MGI:97622; Pln.

DR InterPro; IPR05984; P lamban.

DR Pfam; PF06472; Phospholamban; 1.

DR Pfam; PF06472; Plnaban; 1.

DR TIGRRAMS; TIGRO1294; P lamban; 1.

TRANSMEM 1 31 CYTOPLASINC (POTENTIAL).

FT DOMAIN 2 52 ACETYLATION (BY SIMILARITY).

TRANSMEM 32 1 ACETYLATION (BY SIMILARITY).

TO PHOSPHORYLATION (BY EXA) (BY SIMILARITY).

SIMILARITY).

SIMILARITY).

7.3601F76A854D3 CRC64;

7.46aps
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MEDLINE=87316936; PubMed=3628007;
Uyeda A., Klano K., Fujii J., Kadoma M., Tada M., Tanaka S.;
"The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-C.familiaris;
MEDLINE-86323152; PubMed=3753485;
Fujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
Fujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
Fujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
Fujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
Fujii J., Kadoma M., Tada M., Toda M., Toda H., Sakiyama F.;
Fujii J., Kadoma M., Tada M., Tada M., Sakiyama F.;
Fujii J., Kadoma M., Tada M., Tada M., Sakiyama F.;
Fujii J., Kadoma M., Tada M., Tada M., Sakiyama F.;
Fujii J., Kadoma M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada M., Tada 
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823, 9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-87083954; PubMed-3793929;
Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Tada M.;
"Complete complementary DNA-derived amino acid sequence of canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-C.familiaris;
MEDLINE-87008549; PubMed=3759968;
Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07) Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB)
                                                                                                                                                                                                                                                                                                                                                                                                                                           93.4%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiac phospholamban.";
J. Clin. Invest. 79:301-304(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEKVOYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEKVOYLTRSAIRRA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=C.familiaris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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P07473;
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SEQUENCE
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                                                                                                                                                                                    SPECIES=Pig; TISSUE=Smooth muscle; MEDLINE=90056437; Pubmed=2530978; Verboomen H., Wuytack F., Eggermont J.A., de Jaegere S., Waistiaen L., Raeymaekers L., Casteels R.; "CDNR, cloning and sequencing of phospholamban from pig stomach smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                  Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R., Phosphorylation Phosphorylation in intact ventricles. Phosphorylation of serine 16 and threonine 17 in response to beta-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                       Discoler. J. 262:353-356(1989).

-! FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.
-! SUBDNIT: Homopentamer.
-! SUBGELIULAR LOCATION: Membrane.
-! TISSUE SPECIFICITY: Heart.
-! TISSUE SPECIFICITY: Heart.
-! PIM: Phosphorylated in response to beta-adrenergic stimulation.
-! SIMILARITY: Belongs to the phospholamban family.
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PIR; A29002; A29002.

PIR; A0540; S05540.

PDB; 1FNK; 06-SPP-00.

InterPro; IPR005984; Plamban.

Pfam; PR0472; Phospholamban; 1.

TIGREAMS; TIGR01294; Plamban; 1.

TIGREAMS; TIGR01294; Plamban; 1.

CYTOPLASMIC (POTENTIAL).
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Pred. No. 4.6e-06;
1; Mismatches 0; Indels
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PHOSPHORYLATION (BY CAMK1).
076361D9ADC424D3 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
28-PRB-2003 (Rel. 41, Last annotation update)
Cardiac phospholamban (PLB).
                                                                                            mulation.";
Biol. Chem. 264:11468-11474(1989).
MEDLINE=89291905; PubMed=2544595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, M16012; AAA30884.1; -.
EMBL; Y00399; CAA68461.1; -.
BMBL; M35393; AAC41618.1; -.
EMBL, X15075; CAA3171.1; -.
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93.3%;
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Matches 14; Conservative
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                                                                                                                                                          SEQUENCE FROM N.A.
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NCBL_TaxID=9031;
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P26677:
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PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
PHOSPHORYLATION (BY CAMK) (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- TISSUE SPECIFICITY: Heart.
-1- FIM: Phosphorylated in response to beta-adrenergic stimulation.
-1- SIMILARITY: Belongs to the phospholamban family.
                                                                                                                                                                                                                           f. Biol. Chem. 266:5375-5383(1991).
-!- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.
-!- SUBGINIT: Homopentamer.
-!- SUBGINITAR LOCATION: Membrane.
SEQUENCE FROM N.A.
MEDLINE=91170195; PubMed=1825996;
Toyofuku T., Zak R.;
"Characterization of CDNA and genomic sequences encoding a chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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MEDLINE=21477403; PubMed=11572948;
Ownes S.; Ireda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M.; Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Pred. No. 7.1e-06;
2; Mismatches 0; Indels
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PIR; 733535; A33535.
HSSP, P26678; 1PLP.
InterPro; IPR005984; P. lamban.
InterPro; IPR005984; P. lamban; 1.
TIGRPAMS; TIGR01294; P. lamban; 1.
TIGRPAMS; TIGR01294; P. lamban; 1.
Transmembrane; Phosphorylation; Acetylation.
31 CYTOPLASMIC (POTENTIAL).
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
50S ribosemal protein L19.
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Matches 13; Conserv
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AC 082074;
DT 15-MAR-2004 (FDT 15-MAR-2004 (FDT 15-MAR-2004 (FDT 15-MAR-2004 (FDT 15-MAR-2004 (FDT 15-MAR-2004 (FDT 15-MAR-2004 (FDT 15-MAR-101-3)
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SPECIES=S.lividans; STRAIN=TK21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 burgdorferi.
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                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                           Gaps
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MEDLINE-21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murrphy L., Oliver K., O'Neil S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.3%; Score 42; DB 1; Length 116; 43.8%; Pred. No. 0.85; Live 6; Mismatches 3; Indels
                       STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13186 MW; 47081773B07F6EB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae, Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
50S ribosomal protein Li9.
RPLS OR SCOSS95 OR SCZE1.12.
Streptomyces coelicolor, and
Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP, MF_00402; ; I. InterPort InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort | InterPort 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP005031; BAC70351.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEKVOYLTRSAIRRAE 16
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81 VEKIELVTRGDVRRAK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribosomal protein; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 43.00
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hopwood D.A.;
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RL19_STRCO
ID _RL19_ST
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Parro V., Mellado R.P.;
Submitted (FBB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCIION: This protein is located at the 30S-50S ribosomal subunit
interface and may play a role in the structure and function of the
aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINS-ATCS 35210 / B31;
MEDLINE-88065943; PubMed-9403685;
Fraser C.M., Caejens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Kerchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S.,
Fanson M.,
Utterback T., Wathey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.3%; Score 42; DB 1; Length 116; 43.8%; Pred. No. 0.85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37D782C6763D0A90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O51642;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP, MF 00402; -; 1.
InterPro, IPR01857; Ribosomal L19.
Pfam; PP01245; Ribosomal L19, 1.
PRINTS; PR00561; RIBOSOMALL19.
ProDom; PD002979; Ribosomal L19; 1.
TIGRFAMS; TIGRO1024; FISLS Sact; 1.
PROSITE: PS01015; RIBOSOMAL L19; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 116 AA; 13142 MW; 37D782C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
                                                                                                                                                                                                                                                                                                                                                                EMBL; AL939124; CAA19387.1; -.
EMBL; Z86111; CAB06800.1; -.
PIR; T34780; T34780.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.8%;
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Best Local Similarity 43.0%
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     o;
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matters G.L., Beale S.I.,
"Structure and expression of the Chlamydomonas reinhardtii alad gene
encoding the chlorophyll biosynthetic enzyme, delta-aminolevulinic
acid dehydrataes (porphobilinogen synthase).";
plant Mol. Biol. 27:607-617(1995).
-! - CATALYTIC ACTIVITY: 2 5-aminolevulinate = porphobilinogen + 2
                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Objects 2017 (Rel. 35, Created) (1-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last sequence update) Delta-aminolevulinic acid dehydratase, chloroplast precursor (EC 4.2.1.24) (Forphobilinogen synthase)
                                                                                                                                                                                                                                                                                                                             53.9%; Score 41; DB 1; Length 121; 50.0%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                      HAWAP, MECO402; -; 1.
InterPro: IPR01857; Ribosomal_L19.
Pfam; PF01245; Ribosomal_L19; 1.
Prom; PF00064; RIBOSOWALL19; 1.
ProDom; PD002979; Ribosomal_L19; 1.
TIGRPAMs; TIGR01024; rpls bact; 1.
TIGRPAMs; TIGR01024; rpls bact; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 121 AA; 14011 MW; A33F7BIE4DF24070 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Porphyrin biosynthesis; second step.

-!- SUBUNT: Homoccaemer (Bp sindlarity).

-!- SUBCELLUTAR LOCATION: Chloroplast.

-!- SIMILARITY: Belongs to the ALADH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U19876; AAA79515.1; -.
PIR; S23487; S23487.
HSSP; P05373; LAWE.
INTERFOO; IPRO01731; AlaD_dehydratase.
Pfam; PRO0149; ALAD, I.
PRINTS; PRO0144; DALDHYDRTASE.
PRODOM; PD002304; AlaD_dehydratase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95201253; PubMed=7894023;
                                                                                      EMBL; AE001170; AAC67044.1; -. PIR; B70187; B70187.
                                                                                                                                                                                                                                                                                                                                                                                                        1 MEKVQYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                          80 IEKVEVLRRGKVRRAK 95
                                                                                                                                                                                                                                                                                                                                               Local Similarity 50.0
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - !- COFACTOR: Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3055;
                                                                                                                            ; BB0699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHLRE
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                                                                                                                                                                                                                                                                                                            Gaps
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PROSITE; PS00169; D_ALA_DEHYDRATASE; 1.
Propiyrin blosyntheeis; Chlorophyll blosynthesis; Lyase; Magnesium; Chloroplast; Transit peptide.
TRANSIT 1 24 CHLOROPLAST (POTENTIAL).
                                                                                             DELTA-AMINOLEVULINIC ACID DEHYDRATASE. MAGNESIUM-BINDING (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                            ·.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                52.6%; Score 40; DB 1; Length 390; 46.7%; Pred. No. 7.4; ive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.3%; Score 39; DB 1; Length 115; 37.5%; Pred. No. 3.1; tive 6; Mismatches 4; Indels
                                                                                                                                                                                             6114C4E0325A4242 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9EBE9A1B89D3122B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L19.
RPLS OR TTE1457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRPAMS, TIGRO1024; FD13 bact; 1.
PROSITE; PS01015; RIBOSOWAL 119; 1.
Ribosomal protein; Complete_proteome
SEQUENCE 115 AA; 13395 MW; 9EBB9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MP_00402; -; 1.
InterPro; IPR001887; Ribosomal L19.
Pfam; PP01245; Ribosomal L19; 1.
PRINTS; PR00061; RIBOSOMALL19.
ProDom; PD002979; Ribosomal L19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE013104; AAM24679.1; -.
                                                                                                                                                                                                390 AA; 43045 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEKVOYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                      198 ETIEYLCROAVSOAE 212
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                                                                                                                                                                                                                                                                                                                                                                      2 EKVQYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                 Local Similarity 46.7 nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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190
312
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                  ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                         Query Match
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                                                                                                               CHAIN
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RL19_THEIN
      SEFFFFS
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       196 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rissum=Brain;
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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HELIX
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STRAND
TURN
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SN29 HUMAN
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TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Crystal structure and induction mechanism of AmiC-AmiR: a lighand-regulated transcription antitermination complex."; EMBO J. 18:5775-5186(1999) EMBO J. 18:5775-5186(1999) and a stranscription and infortermination is aliphatic amidase. Acts as a transcriptional antitermination factor. It is thought to allow RNA polymerase read through a rhoindependent transcription terminator between the amiB promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PAC1;
MEDLINE=99437995; PubMed=10508151;
O'Hara B.P., Norman R.A., Wan P.T., Roe S.M., Barrett T.E., Drew R.E.,
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDINE=2043737 PubMed=10984043;

MEDINE=2043737 PubMed=10984043;

Stover C.K., Pham X.-O.T. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Santh K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Nature 406:959-964(2000)."
                                                                                                                                                                                                  MEDLINE-89211409; PubMed=2495988;
Love N., Rice P.M., Drew R.E.;
"Nucleoride sequence of the aliphatic amidase regulator gene (amiR) of Pseudomonas aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson S.A., Drew R.E.; "Transcriptional analysis of the amidase operon from Pseudomonas
                                                                                                                           3acteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF COMPLEX WITH AMIC
                                               01-JUL-1989 (Rel. 11, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
AMIR OR PA3363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Forms a complex with amiC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE004758; AAG06751.1; -.
PIR; B83226; B83226.
PIR; S03884; S03884.
PDB; 1Q00, 23-DEC-99.
PDB; 1Q00, 23-DEC-99.
InterPro; IPR005561; ANTAR.
InterPro; IPR00327; Res_reg_antiterm.
PEam; PF03861; ANTAR; 1.
                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 177:3052-3057(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95286483; PubMed=7539417;
                                                                                                                                       Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X13776; CAA32023.1; -.
                                                                                                                                                                                                                                                    FEBS Lett. 246:39-43(1989).
                        STANDARD;
                                                                                                             Seudomonas aeruginosa.
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                  NCBI_TaxID=287;
                                                                                                                                                                                       STRAIN=PAC433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aeruginosa."
                       AMIR PSEAE
P10932;
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PIRSF) PIRSF036382; Res_reg_antiterm; 1.

Transcription regulation; Transcription antitermination; 3D-structure; Complete proteome.

CONFLICT 48 48 5 -> A (IN REF. 1).

CONFLICT 64 64 R -> G (IN REF. 1).

CONFLICT 141 141 E -> D (IN REF. 1).

CONFLICT 154 154 A -> V (IN REF. 1).

CONFLICT 154 154 A -> H (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last montation update)
8ynaptosomal-associated prorein 29 (SNAR-29) (Wesicle-membrane fusion protein SNAR-29) (Soluble 29 kDa NSF attachment protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S., Luo Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pancreas;
PUDMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.3%; Score 39; DB 1; Length 196; 53.3%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steegmaier M., Yang B., Yoo J.-S., Huang B., Shen M., Yu scheller R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schardt A., Kraemer B.-M., Werner H., Nave K.-A., "Genomic organization of the human SNAP29 gene."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iree novel proteins of the syntaxin/SNAP-25 family.";
Biol. Chem. 273:34171-34179(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21903 MW; 306A4F30E8E4C6C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 258 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99069409; PubMed=9852078;
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166 EAHQYLSREAMKRRE 180
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Ponaldo M.F., Carninci P., Prange C.,
Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
Richards S., Morley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Halles S., Gibbs R.A.,
Richards S., Morley K.C., Halles S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Halles S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hallen S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakes R.W., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chenerh A., Schein J.B., Jones S.J.M., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99;16899-16903 (2002).
-!- FUNCTION: INVOLVED IN WULTIPLE NEMBRANE TRAFFICKING STEPS.
-!- SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAKINS.
-!- SUBCELLULAR LOCATION: APPEARG TO BE MOSTLY MEMBRANE-BOUND,
PROBABLY VIA INTERACTION WITH SYNTAKINS, BUT A SIGNIFICANT PORTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- TISSUE SPECIFICITY: FOUND IN BRAIN, HEART, KIDNEY, LIVER, LUNG, PLACENTA, SKELFRAL MUSCLE, SPIEERD AND PANCERSAS.
-1- SIMILARITY: Belongs to the SNAP-25 family.
-1- SIMILARITY: Contains 1 t-SNARE coiled-coil homology domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INCERTOR JERONOUSZI, TENANE.

PÉRMI, PPO0835; SNAP-25; 1.

PÉRMI, PPO0835; SNAP-25; 1.

SMART, SM00397; t. SNARE; 1.

PROSITE, PSS0192; T. SNARE; 1.

PROSITE, PSS0192; T. SNARE; 1.

Protein transport; Synaptoscome; Coiled coil; Membrane.

Protein transport; Synaptoscome; Coiled coil; Membrane.

Protein transport; Synaptoscome; Coiled coil; Membrane.

Protein transport; Synaptoscome; T. SNARE; 107

COLLED COIL (POTENTIAL).

DOMAIN 196 258 T. SNARE COILED-COIL HOMOLOGY.

SEQUENCE 258 AA; 28970 MW; 7EICDBA22D6FSA3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.3%; Score 39; DB 1; Length 258; 46.7%; Pred. No. 7.3; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005484; F:SNAP receptor activity; TAS.
GO; GO:0006887; P:excytosis; TAS.
GO; GO:0006844; P:emembrane fusion; TAS.
GO; GO:0006949; P:membrane fusion; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 871 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF115436; AAD11436.1; -: EMBL, AR278704; AAF91421.1; -- EMBL, BC0009715; AAH09715.1; -- Genew, HGNC:11133, SNAP29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EKVQYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 DROOYLROEVLRRAE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 46.7% tes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IS CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 604202;
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Q9HJW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; ME_0036; -; 1.
InterPro; IPR002318; tRNN-synt_2c.
InterPro; IPR002318; tRNN-synt_Ala.
Pfam; PF01411; tRNA-synt_2c; 1.
PRINTS; PR00980; TRNASYNTHALA.
TIGRPAMS; TIGRO0344; alas; 1.
PROSTER; PS50860; AA TRNA_LIGASE II ALA; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; AIP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                         Nature 407:508-513(2000).
-!- CATALYTIC ACTYVIY: ATP + L-alanine + tRNA(Ala) = AMP +
diphosphate + L-alanyl-tRNA(Ala).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Rewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.,
"The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _150/2021).
Involved in the transcription termination process (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                       Thermoplasma acidophilum.
Archaea, Euryarchaeota, Thermoplasmata, Thermoplasmatales;
Thermoplasmataceae, Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.3%; Score 39; DB 1; Length 871; 69.2%; Pred. No. 27; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
N utilization substance protein B homolog (NuSB protein).
NUSB OR ILLO787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechococcus elongatus (Thermosynechococcus elongatus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               871 AA; 99907 MW; 6A6B55478463666D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Chroccoccales; Synechococcus.
NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL445065; CAC11978.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 KVGYLARMLIRRA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KVQYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 69.2
Matches 9, Conservative
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                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome
SEQUENCE 871 AA
                                                                                                                NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    simijarity).
ALAS OR TA0849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUSB SYNEL
ID NUSB SYNEL
AC Q8DKS0;
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-56276417; PubMed-8694763; Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I., Merlevede W., Goris J., Hemmings B.A.; "The variable subunit associated with protein phosphatase 2A0 defines a novel multimember family of regulatory subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
MEDLINE=96355607; PubMed=8703017;
MCCTight B., Rivers A.M., Audin S., Virshup D.M.;
MCCTight B., Rivers A.M., Audin S., Virshup D.M.;
mccright B., Rivers A.M., Audin S., Virshup D.M.;
mccright B., Rivers A.M., Audin S., Virshup D.M.;
mccright B., Rivers A.M., Audin S., Virshup D.M.;
encodes differentiation-induced phosphoproteins that target PP2A to both nucleus and cytoplasm.";
J. Biol. Chem. 271:22031-22039(1996).
J. Biol. Chem. 271:22031-22039(1996).
FINCTION: The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCright B., Virshup D.M., "Identification of a new family of protein phosphatase 2A regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OTT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein phosphatases 2A, 56 kDa regulatory subunit,
alpha isoform (PP2A, B subunit, B' alpha isoform) (PP2A, B subunit,
B56 alpha isoform) (PP2A, B subunit, PR61 alpha isoform) (PP2A, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBŪNIT: PP2A consists of a common heterodimeric core enzyme, composed of a 36 kDa catalytic subunit (subunit C) and a 65 }
                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                 50.0%; Score 38; DB 1; Length 212; 43.8%; Pred. No. 9.1; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 47-56; 129-132; 347-354; 448-462 AND 471-480
                                                                                                                                                        EMAMP, MP 00075, -; 1.
InterPro; IPRO06027; NuBB.
Pfam; PF01029; NusB; 1.
Transcription termination; Complete proteome.
SEQUENCE 212 AA; 24086 MW; FADF36B9391D82CO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   486 AA,
 - !- SIMILARITY: Belongs to the nusB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 270:26123-26128(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Breast cancer;
MEDLINE=96064678; PubMed=7592815;
                                                                                                                                              EMBL; AP005371; BAC08338.1; -.
                                                                                                                                                                                                                                                                                                              1 MEKVOYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                                                                :|| | : : |::|||
74 LEKAQMVLQDALQRAE 89
                                                                                                                                                                                                                                                                 ilarity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit, R5 alpha isoform).
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     compartment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                2A5A HUMAN
Q15172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunits."
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPP2R5A
                                                                                                                                                                                                                                                                                                                                                                                                     2ASA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0008601; F:protein phosphatase type 2A, intrinsic regu. . .; TAS. InterPro; IRRO0893B; ARM. InterPro; IRR002554; B56. Pfam; PF01603; B56; 1.
constant regulatory subunit (PR65 or subunit A), that associates with a variety of regulatory subunits. Proteins that associate with the variety of regulatory subunits broteins that associate with the variety of regulatory subunits B (the R2/B/R85/B55, R3/B''/PR12/R8130/PR59 and R5/B'/B56 families), the 48 kDa variable regulatory subunit, viral proteins, and cell signaling molecules.
-!- SUBCELLULAR LOCATION Cytoplasmic.
-!- TISSUE SPECIFICITY: Widely expressed with the highest expression in heart and skeletal muscle.
-!- PTM: Phosphorylated on serine residues.
-!- SIMILARITY: Belongs to the phosphatase 2A regulatory subunit B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88298841; PubMed=3042778;
Acharetter T., Franzusoff A., Field C., Schekman R.;
"SECT encodes an unusual, high molecular weight protein required for membrane traffic from the yeast Golgi apparatus.";
J. Biol. Chem. 263:11711-11717(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
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H -> S (IN REF. 2; AA SEQUENCE).
F -> E (IN REF. 2; AA SEQUENCE).
D31407F7032A6D44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 486; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murphy L., Harris D.E., Barrell B.G., Rajandream M.A.; Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2009 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF01603; boo; ...
Phosphorylation, Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005737; C:cytoplasm; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 R
56193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [3]
SEQUENCE OF 204-2009 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L42373; AAC37601.1; -. PIR; IS5449; IS5449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-542 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKVDGFTRKSVRKAQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 46...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:9309; PPP2R5A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 4
486 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
SEC7_YEAST
ID SEC7_YEAST
                                                                                                                                                                                                                                                                                                   family
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124

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50S ribosomal protein L19
                                                                                                                                         FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                SEQUENCE
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                        RPLS OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBNNZO,
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RL19_CORGL
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                MEDLINE=91093340; PubMed=1986005; Praller R.S., Schekman R.; Franzusoff A., Redding K., Crosby J., Fuller R.S., Schekman R.; Localization of components involved in protein transport and processing through the yeast Golgi apparatus."; J. Cell Biol. 112:37-37(1991).
-!- FUNCTION: May play a role in vesicular budding and traffic between compartments of the Golgi apparatus.
-!- SUBCELLULAR LOCATION: Cytoplasmic; associated with the peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 246727; CAA86696.1; --
EMBL; 246727; CAA86696.1; --
FIR; 249764; 249764.

FIR; 249918; 1PBV.

Germonline; 140661; --
SQD; S0002577; SRC7.

GO; GO:0005770; C:Qtosol; IDA.

GO; GO:0005789; C:Qtosol; IDA.

GO; GO:0005780; C:Ate endosome; IDA.

GO; GO:0005880; F:ARF guanyl-nucleotide exchange factor activity; IDA.

GO; GO:0006888; P:ER to Golgi transport; IMP.

GO; GO:0006881; P:Intra-Golgi transport; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                   Golgi membrane.
--- DOMAIN: The highly charged acidic domain may serve a structural role to interact with lipids or proteins on the cytoplasmic surface of the Golgi apparatus.
--- PTM: Phosphorylated.
--- SIMILARITY: Contains 1 SEC7 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein transport, Golgi stack, Phosphorylation.
89 213 ASP/GLU-RICH (HIGHLY ACIDIC).
824 1010 SEC7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 2009;
Pred. No. 1e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oliver K., Harris D., Barrell B.G., Rajandream M.A., Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 43, Created)
(Rel. 43, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J03918; AAB04031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
ilarity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008938; ARM.
InterPro; IPR000904; Sec7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                668 VDYLTRLALTRVE 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01369; Sec7; 1.
SMART; SM00222; Sec7; 1.
PROSITE; PS50190; SEC7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VOYLTRSAIRRAE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                   CHARACTERIZATION.
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15-MAR-2004
15-MAR-2004
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ID RL19 COREF
AC Q8FP56;
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CONFLICT
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SEQUENCE
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  SOLUTION NEW TRANSPORTANT NEW TOOLS OF THE TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT NEW TRANSPORTANT N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a rolle in the structure and function of the aminoacy1-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                           STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDINE=2723782; PubMed=1284036;
Mishio Y., Nakamura Y., Kawaraboyasi Y., Usuda Y., Kimura E., Sugimoto, S., Marsul K., Yamagishi A., Kikuchi H., Ikeo K.,
Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cornebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynèbacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.7%; Score 37; DB 1; Length 113; 37.5%; Pred. No. 7.2; tive 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9BD1C9D25ADA453A CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 AA.
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; NP_00402; ; 1.
InterPto. IPROUBS7; Ribosomal L19.
Fiam; PF01245; Ribosomal L19. 1.
PRINTS; PR00661; RIBOSOMALL19.
ProDom; PD002579; Ribosomal L19; 1.
IGREAMS; TIGRO1024; rp18_bct; 1.
PROSITE; PS01015; RIBOSOMAL L19; 1.
PROSITE; PS01015; RIBOSOMAL L19; 1.
Ribosomal protein; Complete_proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP005220; BAC18742.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 13:1572-1579(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AA; 13008 MW;
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Matches 6; Conservative
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                                                                                                                      NCBI_TaxID=152794;
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MEDLINE=21456156; PubMed=11572479;

NEMEDLINE=21456156; PubMed=11572479;

NEMETABAYSAI Y., Hinto Y., Horrikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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                                                                                                                                                                                                                                                                                                                                                                                          48.7%; Score 37; DB 1; Length 113; 37.5%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of an aerobic thermoacidophilic Crentarchaeon, Sulfolobus tokodaii strain7."; DNA Res. 8:123-140(1201).
-!- SIMILARITY: Belongs to the UPP0189 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                   4, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_01205; -; 1.
InterPro; IPR002589; Alpp.
Pfam; PF01661; Alpp; 1.
Hypothetical of Alpp; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 182 AA; 20183 MW; 1E0A072586AF8947 CRC64;
                                                                                                                                                                                                                                                                                                                                                      2692B361BAFBA229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 41, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                           HAMAP; NP_00402; -; 1.
InterPro.; IRROD1857; Riboscmal_L19.
Fram; PF01245; Riboscmal_L19; 1.
PRINTS; PR00061; RIBOSCMALL19.
PPODOM; PD02979; Riboscmal_L19; 1.
ITGREAMS; TIGRO1024; PD1S bact; 1.
PROSITE; PS01015; RIBOSCWAL,L19; 1.
Riboscmal protein; Complete_protecme.
SEQUENCE 113 AA; 12875 MW; 26928361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP000989; BAB67492.1; -.
                                                                                                                                                                          EMBL; AP005280; BAB99430.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEKVQYLTRSAIRRAE 16
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80 IEKIEVIRRGDVRRAK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein ST2383.
                                                                                                                                                                                                                                                                                                                                                                                                              37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus tokodaii
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBL_TaxID=111955;
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28-FEB-2003
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                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
examining the role of niche-specific genes in the evolution of the
examining the role of niche-specific genes in the evolution of the
chamydiaceae.";

Nucleic Acids Res. 31:2134-2147(2003)
-!- CATALYTIC ACTIVITY: Phosphatidyl-L-serine =
phosphatidylethanolamine + CO(2).
-!- COFACTOR: Pyruvcyl group (By similarity).
-!- COFACTOR: Pyruvcyl group (By similarity).
-!- SIMILARITY: Belongs to the phosphatidylserine decarboxylase
family. Subfamily 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN (BY SIMILARITY).
PHOSPHATIDYLSERINE DECARBOXYLASE ALPHA
CHAIN (BY SIMILARITY)
CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY
CONVERTED TO A PYRUVOYL GROUP (BY
                                                                                                                                                                                                                                                        10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Phosphatidylserine decarboxylase proenzyme (BC 4.1.1.65) [Contains: Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine decarboxylase alpha chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phospholipid biosynthesIs, Lyase, Decarboxylase, Pyruvate, Zymogen, Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=22569155; PubMed=12682364; Melson W.C., Faulsen I.T., Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Faulsen I.T., Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A., Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHATIDYLSERINE DECARBOXYLASE BETA
                                                                                                                                                                                                                                                                                                                                                                                       Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila
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                48.7%; Score 37; DB 1; Length 182;
46.7%; Pred. No. 12;
iive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.7%; Score 37; DB 1; Length 299; 50.0%; Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAD, MF 00663; -; 1.
InterPro; IPR003817; PS Dcarbxylase.
InterPro; IPR00521; PS decarb.
Pfan: PF20266; PS Dcarbxylase; 1.
TIGRFAMS; TIGR00163; PS_decarb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE016997; AAP05666.1; -.
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                                                                                                              90 EKLEEAIRNALRKAE 104
                                                                                          2 EKVQYLTRSAIRRAE 16
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Overy Match
Best Local Similarity 46.7*
Best Local 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=83557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
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                                                                                                                                                                                   RESULT 19
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0
                                                                                                                                                                                                                                                                            Pyrococcus furiosus.
Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
-:- PATHWAY: Glycerol utilization; first (rate-limiting) step.
-:- SIMILARITY: Belongs to the fucokinase / gluconokinase / glycerokinase / xylulokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-VCI / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrcoccus furiosus genome.";
Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Key enzyme in the regulation of glycerol uptake and
                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
(Glycerokinase) (GK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glycerol kinase (RC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
(Glycerokinase) (GK),
GLPK OR PYRABO2670 OR PAB2406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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43.8%; Pred. No. 34;
tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PSO0933; FGGY KINSES_1; 1.
PROSITE, PSO0933; FGGY KINASES_1; 1.
PROSITE, PSO0445; FGGY KINASES_2; 1.
Glycerol metabolism; Transferase; Kinase; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 490 AA; 55046 MW; 60A0BBB0EE297A3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (PROBABLE).
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490 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAD; MF_00186; -; 1.
InterPro; IPR000577; FGGY kin.
InterPro; IPR00599; Glycerol_kin.
Pfam; PF00370; FGGY c; 1.
Pfam; PF02782; FGGY c; 1.
TIGRFAMS; TIGR01311; glycerol_kin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE010293; AAL82128.1; -.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolism.
                                                                                                                                                                                                                                               GLPK OR PF2004
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Q9V207;
PYRFU
                                                                                                                                                                                                                                                                                                                                                  Pyrococcus,
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                                                                                          STRAIN=GES / Orsay;
MEDIINE=22511545; PubMed=12622808;
Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.,
"An integrated analysis of the genome of the hyperthermophilic archaeon.Pyrococcus abysi,"
Mol. Microbiol. 47:1495-1512(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Magnesium-chelatase subunit chlD (Mg-protoporphyrin IX chelatase) (Mg-chelatase subunit D).
Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
-!- PATHWAX: Glycerol utilization; rate-limiting step.
-!- SIMILARITY: Belongs to the fucokinase / glycerokinase / xyulokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maguda T., Nakayama M., Ohta H., Takayama K.-I., "Cloning and sequencing of a chlD gene encoding a subunit of magnesium-chelatase from the cyanobacterium Synechococcus sp. PCC
                                                                                                                                                                                                                                             -!- FUNCTION: Key enzyme in the regulation of glycerol uptake and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.7%; Score 37; DB 1; Length 494; ilarity 43.8%; Pred. No. 35; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERSP. POBSES, 101.
HSSP. POBSES, 101.
HSSP. POBSES, 101.
HSSP. POBSES, 101.
HSSP. POBSES, 101.
HAWAP, MF_00186; -; 1.
InterPro; IPR00557; FGGY kin.
InterPro; IPR005599; Glycerol_kin.
Pfam; PF00518; PGGY; 1.
Pfam; PF00518; PGGY; 1.
TIGREAMS; TIGR01311; Glycerol_kin; 1.
PROSITE; PS009331; PGGY_KINASES_1; 1.
PROSITE; PS009445; PGGY_KINASES_2; 1.
Glycerol_metabolism; Transferase; Kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 AA; 55692 MW; D868694AF74E8CC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ248283; CAB49191.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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nes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
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                                                                          SEQUENCE FROM N.A.
                                        NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=1140;
                                                                                                                                                                                                                                                                    metabolism.
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007345;
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TISSUE=Cervical carcinoma;

MEDLINE=98234402; PubMed=9566967;

Murphy S.M., Urbani L., Stearns T.;

"The mammalian gamma-tubulin complex contains homologues of the yeast spindle pole body components spc97p and spc98p.";

J. Cell Biol. 141:663-674(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 098572; 043632;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CFT-2003 (Rel. 42, Last annotation update)
damma-rubulin complex component 2 (GCP-2) (Spindle pole body protein
Spc97 homolog) (hSpc97) (hGCP2) (h103p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
-!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                      -!- PATHWAY: Chlorophyll biosynthesis.
-!- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
-!- SIMILARITY; Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.7%; Score 37; DB 1; Length 677; 47.6%; Pred. No. 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01078; Mg_chelataes, 1.
Pfam; PF001078; Waa; 1.
SWART; SM00327; WAA; 1.
SWART; SM00327; WAA; 1.
PROSITE; PS50224; WRA; 1.
Photosynthesis; Chorophyll biosynthesis; ATP-binding.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 383 GLU/PRO-RICH.
677 AA; 73367 MW; 7E2988E096DF5506 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 902 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB003135; BAA20346.1; -.
InterPro; IPR003593; AAA AIPase.
InterPro; IPR00523; Mg_Chelatse_chII.
InterPro; IPR002035; VWF_A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 EQIGYLVREAIRGOVOGHRAE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EKVQYLTRSAIR-----RAE 16
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Local S...
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SEQUENCE
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       SO THE STREET BRANKER OF THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE SO THE S
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensegisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:185>9; 10001259; 20098.
Interbro; IPRO/7259; 20097_Spc98; 1.
Microtubule; Alternative splicible.
DOMAIN 109 112 POLY-ALA.
VARSPLIC 513 560 IABIARR-> PGPSSATSSWIPRATSSCTSWIFRRESGSR WRISPLIC 513 WRISPLIA -> PGPSSATSSWIPRATSSCTSWIFRRESGSR WRISPLAWRSWIPRA (in isoform 2).
                                                                                                                                                                                                                                                                                                                                          nucleation at the centrosome.
--- SUBUNIT: Gamma-tubulin complex is composed of gamma-tubulin, GCP2, GCP5 and GCP6.
--- SUBUSILUTAR LOCATION: Centrosome.
--- ALTERNATIVE PRODUCTS:
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Youdhan A., Shevchenko Y., Boufferd G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones M.J., Marza M.A., Schein J.E., Jones M.J., Marza M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences"; proceedings of more than 15,000 full-length human and mouse CDNA sequences"; proceedings of more than 15,000 full-length human and mouse LDNA sequences"; proceedings of more than 15,000 full-length human and mouse LDNA sequences"; proceedings of more than 15,000 full-length human and mouse LDNA sequences"; proceedings of more chan 15,000 full-length human and mouse LDNA sequences"; proceedings of more chan 15,000 full-length human and mouse LDNA sequences"; proceedings of more chan 15,000 full-length human and mouse LDNA sequences"; proceedings of more chan 15,000 full-length human and mouse LDNA sequences"; proceedings of more chan 15,000 full-length human and mouse LDNA sequences"; proceedings of more chan 15,000 full-length human and mouse LDNA sequences"; proceedings of more chan 15,000 full-length human and mouse LDNA sequences"; proceedings of more chan 15,000 full-length human and mouse LDNA sequences"; proceedings of more changed that the control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more control of the more 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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Best Local Similarity 53.3%; Pred. No. 66;
Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      902 AA; 102533 MW; 4FAAF864A3758E6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoid=Q9BSJ2-2; Sequence=VSP_001617, VSP_001618,
Note=No experimental confirmation available;
-!-TISSUE SPECIFICITY: Ubiquitously expressed.
-!- SIMILARITY: Belongs to the GCP family.
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/FIId=VSP 001617.
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
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01-AUG-1992 (Rel. 23, Last sequence update)
28-FES-2003 (Rel. 41, Last annotation update)
Hexokinase type III (EC 2.7.1.1) (HK III).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=09BSJ2-1; Seguence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BC005011, AAH05011.1, -.
Genew, HGNC:18599, TUBGCP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF042379; AAC39728.1; -.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2
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ID HXK3_RAT
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                                                                                                                                                                                                                                                                                                                                           White J.A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
-!- ENZYME REGULATION: Hexokinase is an allosteric enzyme inhibited by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: First step of several metabolic pathways.
-!- SUBUNIT: Monomer.
-!- SUBUNIT: Monomer.
-!- DOMAIN: THE N- AND C-TERMINAL HALVES OF THIS HEXOKINASE SHOW EXTENSIVE SEQUENCE SIMILARITY TO EACH OTHER. THE CAPALYTIC FUNCTION IS ASSOCIATED WITH THE N-TERMINUS.
-!- MISCELLANEOUS: In vertebrates there are four major glucosephosylating isoenzymes, designated hexokinase I, II, III and
                         MEDLINE=91378267; PubMed=1897938; Schwab D.A., Wilson J.B.; Schwab D.A., Wilson J.B.; Complete amino acid sequence of the type III isozyme of rat hexekinase, deduced from the cloned cDNA."; Arch. Blochem. Blophys. 285:365-370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00475; HEXOKINASE.
PRODOM; PD001109; Hexokinase; 2.
PROSITE; PS00379; HEXOKINASES; 2.
Transferase; Kinase; Glycolysis; Allosteric enzyme; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.7%; Score 37; DB 1; Length 924; 53.3%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUCOSE-BINDING (POTENTIAL). GLUCOSE-BINDING (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the hexokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NCV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histone H4 (Fragment).
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InterPro; 1PR001312; Hexokinase.
Pfam; PP03727; hexokinase2; 2.
Pfam; PP00349; hexokinase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100253 MW;
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Best Local Similarity 53.2.
Best Local Similarity
Arrange St. Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      its product Glc-6-P.
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924 AA;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE
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Blepharisma japonicum. Eukaryota, Alveolata, Ciliophora, Heterotrichea, Heterotrichida, Blepharismidae, Blepharisma.

NCBI TaxID=5961;

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MEDLINE-9725756; PubMed-9103980; MEDLINE-9725756; PubMed-9103980; MEDLINE-9725756; PubMed-9103980; MEDLINE-9725756; PubMed-910380; Medicine in the macronucleus of Blepharisma japonicum (Protozoa, Ciliophora, Heterotrichida)."; PEMS Microbiol. Lett. 149:93-98 (1997).

1- FUNCTION: Histone H4, along with histone H3, plays a central role in nucleosome formation.

1- SUBUNT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                         -!-SIMILARITY: Belongs to the histone H4 family.
InterPro, IPR001951; Histone_H4.
PRINTS; PR00623; HISTONEH4.
ProDom; PD001827; HISTONEH4; 1.
PROSITE; PS00047; HISTONE_H4; PARTIAL.
Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description                   | Q82jw4 streptomyce | Q8dbn7 vibrio vuln | Q9rev7 pseudomonas | Q8wm34 ursus marit | Q974n9 sulfolobus | Q9ar53 volvox cart |        | Q9dbc5 mus musculu |        | Q9q6q3 grapevine l | Q8cfm4 mus musculu | Q87gq3 vibrio para | 058310 pyrococcus | Q9ufe6 homo sapien | homod  | 095213 homo sapien |
|-----------|-------------------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|
| SUMMARIES |                               | W4                 | N.7                | 77                 | 4                  | 6N                | 53                 | 26     | Ċ5                 | BO     | 83                 | Μ4                 | Š                  | 10                | وب                 | 7      | е                  |
| S         | ID                            | Q82JW4             | OBDBN.             | Q9REV              | QBWM34             | Q974N9            | Q9AR5              | 09JIS6 | Q9DBC              | Q9ERB( | 09060              | QBCF               | 087603             | 05831             | Q9UFE6             | CITN60 | 095213             |
|           | DB                            | 16                 | 16                 | 16                 | 7                  | 17                | 10                 | 11     | 11                 | 11     | 12                 | 11                 | 16                 | 17                | 4                  | 4      | 4                  |
|           | %<br>Query<br>Match Length DB | 116                | 527                | 417                | 79                 | 122               | 212                | 257    | 260                | 260    | 527                | 998                | 1104               | 1108              | 452                | 1027   | 1120               |
|           | ery                           | 5.3                | 5.3                | 3.9                | 9.2                | 5.6               | 9.2                | 5.6    | 5.6                | 5.6    | 9.2                | 5.6                | 5.6                | 2.6               | 2.0                | 0.2    | 2.0                |
|           | * 58                          |                    | ហ                  | S                  | S                  | w                 | ហ                  | ហ      | Ŋ                  | 'n     | Ŋ                  | ß                  | 'n                 | S                 | S                  | ហ      | ιú                 |
|           | Score                         | 42                 | 42                 | 41                 | 40                 | 40                | 40                 | 40     | 40                 | 40     | 40                 | 40                 | 40                 | 40                | 39.5               | 39.5   | 39.5               |
|           | Result<br>No.                 | Н                  | 7                  | m                  | 4                  | Ŋ                 | φ                  | 7      | œ                  | σ'n    | 10                 | 11                 | 12                 | 13                | 14                 | 15     | 16                 |

| Q96fr06 homo sapien Q96we8 homo sapien Q90x93 meacaca neme Q90x93 streptococo Q868u8 lil pseudomonas Q9v1d2 pyrocococus Q868u8 euplotes ae Q7x459 oryza sativ Q89j03 bradythizob Q97bd7 thermoplasm Q84675 chlamydia p Q97bd7 thermoplasm Q84675 chlamydia p Q97bd7 thermoplasm Q84675 chlamydia p Q97bd7 thermoplasm Q84675 chlamydia p Q97bd7 thermoplasm Q84675 chlamydia p Q97bd7 thermoplasm Q84675 chlamydia p Q97bd7 pantoplac Q810979 pantoploc Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pan troglod Q30978 pantoploc Q30978 pantoploc Q30978 pantoploc Q30978 pantoploc Q30978 macaca mula Q84yi3 bifidobacte Q8ywsi anabaena sp Q9xds anabaena sp Q9xds anabaena sp Q9xds anabaena sp Q9xds arabidobacte Q8xdf orsophila Q9vdis drosophila Q9vdis drosophila Q9vdis blepharisma G61183 blepharisma G61183 blepharisma                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 062614 protocruzia 062586 blepharisma p79456 bos taurus 07956 canis famil 07853 canis famil 077853 canis famil 077848 canis famil 077857 canis famil 07557 canis famil 07555 canis famil 077857 canis famil 077857 canis famil 077857 canis famil 077857 canis famil 077858 canis famil 07867 canis famil 0864m8 streptococc 08240 nitrosomona 027875 trichomonas 077875 methanobact 087879 vibrito para 09bcw8 acrocophalu 026701 methanobact 086821 encephalito |
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| 0996806<br>030735<br>030735<br>030735<br>0881L1<br>0881L1<br>0881L1<br>0881L1<br>0881L1<br>0881L1<br>0881L1<br>0881L1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0881B1<br>0 | 062614 0623RV9 0623RV9 0723R56 077855 077853 077857 077857 077857 077857 077857 077857 077857 077857 077857 077857 077857 077857 078772 078772 087772                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
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| 111<br>114<br>115<br>116<br>117<br>117<br>118<br>118<br>118<br>118<br>118<br>118                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| ~~<br>***********************************                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Ა ୦ ୬ ଅ ୬ ୪ ୬ ୬ ୬ ୦ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୩ ୩ ୩ ୩ ୩                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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Q8DBN7

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Q22by5 streptomyce
Q92by2 rhizobium m
Q92x4 arabidopsis
Q94c6 pseudomonas
Q97a1 leptospira
Q97a1 sulfolomos
Q97a3 sulfolobus
Q97ab3 sulfolobus
 Q8xv42 ralstonia s
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In Mat. Biotechnol. 21:526-531(2003).

Rabi, Apor0591; BAC70351.1.

RABI, Apor0591; BAC70351.1.

RO, GO:0005840; C:ribosome, IEA.

CO, GO:0005840; C:ribosome, IEA.

CO, GO:0005840; C:ribosome, IEA.

CO, GO:0005412; P:prottural constituent of ribosome; IEA.

RO, GO:000412; P:prottural constituent of ribosome; IEA.

RO, GO:000597; Ribosomal L19: I.

RINTS; PRO0061; RIBOSOMALL19: I.

RINTS; PRO0061; RIBOSOMALL19: I.

RIGREMA: TIGREDAM: TIGREDAM: ADORT III):

RIGREMA: TIGREDAM: TIGREDAM: ATORIT/3BO7F6EB6 CRC64;

SEQUENCE 116 AA, 13186 MW; 47081773B07F6EB6 CRC64;
               096847 dictyosteli
Q23896 dictyosteli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21477403; PubMed=11572948;
MEDLINE=21477403; PubMed=11572948;
OWLY S., IRAGA H., IShiKawa U., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.3%; Score 42; DB 16; Length 116; 43.8%; Pred. No. 6.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=222608106; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ribosomal protein L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                        PRT; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                          ALIGNMENTS
                                                             Q92P72
Q8GXX4
Q914C6
Q8F7A1
                                              Q82BY5
                 096847
Q23896
                                                                                                                                            297ZB3
                                                                                                                                                          O9HLG9
                                                                                                                             900560
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81 VEKIELVTRGDVRRAK 96
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nes 7; Conservative
                                                                                                                                                                                                                                                                                      PRELIMINARY;
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44444444444

444444444444
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Matches
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RESULT 2

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STRIN-ATCC 15692 / PAO1;
MEDLINE=20431337, PubMed=10984043;
MEDLINE=20431337, PubMed=10984043;
Stover C. K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F. S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Coller D., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Bridk K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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"Analysis of the Pseudomonas aeruginosa hydrogen cyanide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; ProteoĎacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
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                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. Vibrionaceae; Vibrio. Vibrio. Vibrio. Vibrio. Vibrionaceae; Vibrio. Vibrionaceae; Vibrio. Vibrionaceae; Vibrio. Vibrionaceae; Vibrio. Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Vibrio vulnificus CMCP6."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE016802; AA010185.1; -.. GO; GO;0016020; C:membrane; IEA. GO; GO:0016020; C:membrane; IEA. GO; GO:0006935; P:chemotaxis; IEA. GO; GO:0007165; P:chemotaxis; IEA. Interpro; IPR004089; Chmtaxis_transd.
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
HCNC (Hydrogen cyanide synthase HCNC).
HCNC OR PA2195.
527 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
SWART; SM00283; MA; 1.
PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9REV7;
01-MAY-2000 (TrEMBLrel. 13, Created)
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    PRT;
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STRAIN=ATCC 15692 / PAO1;
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    PRELIMINARY;
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nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Vibrio vulnificus.
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    Q8DBN7
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                                          EMBL; AF208523; AAF21001.

EMBL; AE006464; AAG05583.1; -

EMBL; AE0064646; AAG05583.1; -

EMBL; AE0064646; AAG05583.1; -

EMBL; AE006468; AE006583.1; -

GO; GO:000318; F:Glycerol-3-phosphate dehydrogenase complex; IEA.

GO; GO:0004388; F:Glycerol-3-phosphate dehydrogenase activity; IEA.

GO; GO:0004388; F:Glycerol-3-phosphate dehydrogenase activity; IEA.

GO; GO:0006189; F:Glycerol-3-phosphate metabolism; IEA.

InterPro; IPR000477; FAD Gly3P dh.

InterPro; IPR000477; FAD Gly3P dh.

InterPro; IPR000437; PAD Gly3P dh.

InterPro; IPR000437; ProK_lipoprot_S.

PEam; PF01266; DAO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Ursidae, Ursus.
NCBI TaxID=29073;
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Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:959-964(2000).
                                                                                                                                                                                                                                                       53.9%; Score 41; DB 16; Length 417; 53.3%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 7; Length 79;
Pred. No. 10;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                             PRINTS; PRO1001; FADG3PDH.
PROSTIE; PS00013; PROKAR_LIPOPROTEIN; 1.
Complete proteome.
SEQUENCE 417 AA; 45281 MW; 63F5DB8A3118F318 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ursus maritimus (Polar bear) (Thalarctos maritimus).
                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                          154 EQVRWLDREELRRAE 168
                                                                                                                                                                                                                                                                                                      2 EKVQYLTRSAIRRAE 16
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ERVRFLTRSIYNREE 29
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                                                                                                                                                                                                                                                                               8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Best Local Similarity
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Best Local Similarity
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8
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Q8WM34;
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RESULT

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"Algal ALAD is unlikely to be derived from the plastid endosymbiont.";
submitted (APR-2001) to the EMBJ/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 2 5-AMINOLEVULINATE = PORPHOBILINOGEN + 2
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=JOW 10445 / 7;
MEDLINE=214 56156; PubMed=11572479;
MEDLINE=21456156; PubMed=11572479;
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takaniya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
ALA dehydratase (EC 4.2.1.24) (Delta-aminolevulinic acid dehydratase)
(Porphobilinogen synthase) (ALADH) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                    Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%; Score 40; DB 17; Length 122; 37.5%; Pred. No. 16; 14; Indels ive 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7."; DNA Res: 9:123-140(2001).

EMBL; AP000983; BAB65618.1; -. Interpro; IPR008301; UCP016498.

IRSF: IRSP016498; UCP016498.

Hypothetical procein; Complete proteome; SEQUENCE 122 AA; 14467 MW; 988A31A274842EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016829; F:1yase activity; IEA.
GO; GO:0004655; F:1yase activity; IEA.
GO; GO:0006783; P:heme biosynthesis; IEA.
InterPro; IFR01731; AlaD_dehydratase.
Pfam: PF00490; ALAD; AlaD.
                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein ST0620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SÜBÜNIT: HOMOOCTAMER (BY SIMILARITY).
-1- SIMILARITY: BELÖNGS TO THE ALADH FAMILY.
EMBL; AJ310903; CAC36225.1; -.
HSSP; P15002; 184E.
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ProDom; PD002304; AlaD dehydratase; 1.
PROSITE; PS00169; D_ALA_DEHYDRATASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEKVQYLTRSAIRRAE 16
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26 MKKIKYLTEBALMKGD 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 37.58
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                 PRELIMINARY;
                                                                                                                                       Sulfolobus tokodaii
                                                                                                                                                                                      NCBI_TaxID=111955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Volvox carteri.
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Q974N9
ID Q9
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein homolog)
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Q9ERB0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Selective Interaction of Complexin with the Neuronal SNARE Complex. Determination of the Binding Regions.";

Determination of the Binding Regions.";

EMBL; AFPG60577; AFF6917.1;

InterPro; IPR000728; SNAP-25.

InterPro; IPR000727; T_SNARE.

Pfan; PP00835; SNAP-25;

Pfan; PP00835; SNARE: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J; TISSUB=Liver;
MEDLINE=21085660; PubMed=11217851;
MEDLINE=21085660; PubMed=11217851;
Axavai U., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Azakawa I., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20347889; PubMed-10777504;
Pabbs S., Hazzard J.W., Antonin W., Sudhof T.C., Jahn R., Rizo J.,
Passbauer D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.6%; Score 40; DB 11; Length 257; Best Local Similarity 43.8%; Pred. No. 35; Matches 7; Conservative 5; Mismatches 4; Indels
                                                                                        Query Match 52.6%; Score 40; DB 10; Length 212; Best Local Similarity 46.7%; Pred. No. 29; Matches 7; Conservative 4; Mismatches 4; Indels
                    NON TER 1 1 1
SEQUENCE 212 AA; 23195 MW; ACODEBODBEC4329E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART, SM00397, t.SNARE; 2.
PROSITE; PS50192, T.SNARE; 1.
SEQUENCE 257 AA; Z9099 MW; F3A26D63A2FE0718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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  Lyase, Porphyrin biosynthesis.
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20 ETIEYLCRQAVSQAE 34
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SNAP29 OR 1300018G05RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNAP-29 protein.
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Q9JI56;
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

RAWAI J., Shinagawa R., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa R., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa R., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa R., Shibata K., Yoshino M., Ashanaka I.,

Alzawa K., Izawa M., Nishi X., Kiyosawa H., Rasukawa T., Saito R.,

Radora K., Marsuda H.A., Ashburnar M., Baralov S., Casawant T.,

Radora K., Marsuda H.A., Ashburnar M., Baralov S., Casawant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Sakai K., Boffelli D., Bojunga N., Carninci P., de Bonaido M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Brownstein M.J., Hill D., Hofmann M., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbaoh C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitming L.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa K., Kuchl P., Lewis S., Matsuch Y., Mikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldareli R., Barsh G., Blake J., Boffeelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wynghaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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01-MAR-2001 (TrEMBLrel. 16, Lat sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
03-0CT-2003 (TrEMBLrel. 25, Last annotation update)
03-0CT-20018G05RIK protein) (RIKEN cDNA 1300018G05 gene) (SNAP-29
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00397; t. SNARE; 2.
PROSITE; PSS0192; T. SNARE; 1.
SEQUENCE: 260 AA; 29692 MW; DC2A3BC8D604477E CRC64;
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OR 1300018G05RIK.
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InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T_SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNAPE; 1.
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Best Local Similarity 43.0.
7, Conservative
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Q8CFM4
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X MEDLINE-22354683; PubMed=12466851;

A The FANTON Consortium,

A the FANTON Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration of the mouse transcriptome based on functional annotation of the mouse transcriptome based on functional annotation of the Mally and Sale Consolored; Bara148621;

B MELL, AX008722; AAG32076.1;

B EMBL; AX080765; BAR24865.1;

B EMBL; AX039203; BAR24865.1;

B MGJ; MGT: 194724; Snap2s.

B MGJ; MGT: 194724; Snap2s.

B MGJ; MGT: 194724; Snap2s.

B MGS; MRP-25; I SNAP-25;

B MGS; MRP-25; I SNAP-25;

B MGS; MRP-25; I SNARE; I SNARE; I SNARE; I SNAPE;

R PROSITE; PS60192; T_SNARE; I SNARE;

SEQUENCE 260 AA; Z9572 MW; DD813A78C605576F CRC64;
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MEDINE-20141373: PubMed=10675398;

MEDINE-20141373: PubMed=10675398;

MICLOCIGE sequence and organization of ten open reading frames in the genome of Grapevine leftroll-associated virus 1 and identification of three subgenomic RNAs.";

Tof three subgenomic RNAs.";

Gen. Virol. 81:605-615(2000).

MELL, AF19582; AF127784.1;

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003968; F:RNA-directed RNA polymerase.

InterPro: IPR007099; RNA-dep_RNApol2.

InterPro: IPR007094; RNA-pol_BS-PS.

InterPro: IPR007094; RNA-pol_BS-PS.

InterPro: IPR007094; RNA-pol_BS-PS.

RAM: PF00978; RNA-directed RNA-pol_BS-PS.

Pfam: PF00978; RNA-pol_BS-PS.

Pfam: PF00978; RNA-pol_BS-PS.

Pfam: PF00978; RNA-pol_BS-PS.

Pfam: PF00978; RNA-pol_BS-PS.

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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
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Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; Hayashizaki Y.; Hayashizaki Y.; Hayashizaki Y.; Hayashizaki Y.; Hayashizaki A.; Hayashizaki A.; Hayashizaki Y.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki A.; Hayashizaki
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                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RNA-dependent RNA polymerase (Fragment).
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Best Local Similarity 43...
Best Local 7; Conservative
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NCBI_TaxID=47985;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            ISSUE=Lund;
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RP SEQUENCE FROM N.A.

RY STRAIN=RIMD 2210633 / Serotype 03:K6;

RX MEDLINE=22508454; PubMed=12620739;

RA MAKINO K., Oshima K., Kurckawa K., Yokoyama K., Uda T., Tagomori K.,

RA Mijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

RA Yasunaga T., Horda T., Shinagawa H., Hattori M., Iida T.;

RT Genome seguence of Vibrio parahaemolyticus: a pathogenic mechanism

RT distinct from that of V. cholerae.";

RL Lancet 361:743-749(2003).

RL Lancet 361:743-749(2003).

RBBL; AP05088; BAC6565.1; -.

RWBL; AP05088; BAC6565.1; -.

RWBY, PROCHETICAL protein; Complete protecome.

RW Hypothetical protein; Complete protecome.

RN SEQUENCE 1104 AA; 125574 MW; 61C89EE3AB30C5DD CRC64;
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OBCEM4;
O1-MRR-2003 (TrEMBLrel. 23, Created)
O1-MRR-2003 (TrEMBLrel. 23, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Buks musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.
Query Match 52.6%; Score 40; DB 12; Length 527; Best Local Similarity 80.0%; Pred. No. 76; Matches 8; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R., Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC013626, AAH13626.1; -. InterPro; IFR003160; Collagen. Pfam; PF01391; Collagen. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       998 AA; 95451 MW; 2AB4BA953B7084A6 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                     95 GYVVRSAIRR 104
                                                                                                                         5 OYLTRSAIRR 14
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PRT;

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PRELIMINARY;
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09NT17
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Yamamoto S., Sekine M., Baba S. II., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Oteuka R., Nakazawa H., Takaniya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
BMBL, Ap000003, BAA29695.1;
PIR, ST1104; E71104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus horikoshii.
Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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52.6%; Score 40; DB 17; Length 1108;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels (
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R QO; GO:0005524; C:nucleus; IEA.

R QO; GO:0005524; F:ATP binding; IEA.

R QO; GO:0005524; F:ATP binding; IEA.

R QO; GO:000804; F:DNA dependent ATPase activity; IEA.

R QO; GO:0008010; P:Cytokinesis; IEA.

R QO; GO:0005020; P:DNA replication initiation; IEA.

R QO; GO:0005020; P:DNA replication; IEA.

R GO; GO:00050380; Hedgehog hintC.

R InterPro; IPR003586; Hedgehog hintC.

R InterPro; IPR00423; INTEIN.

R InterPro; IPR00424; INTEIN.

R InterPro; IPR00429; MCM.

R InterPro; IPR00442; MCM.

R InterPro; IPR00442; MCM.

R PRINTS; PR00493; MCM.

R PRINTS; PR01659; MCMPALIY.

R PRINTS; PR01659; MCMPALIY.

R PRINTS; PR01650; MCMPALIY.

R PRINTS; RM00306; HintC; 2.

R SMART; SM00306; HintC; 2.

R SMART; SM00306; HintC; 2.

R SMART; SM00306; MCM; 1.

R PROSITE; PS50019; INTEIN.

R PROSITE; PS50019; INTEIN.

R PROSITE; PS5001; MCMPAL; 1.

R PROSITE; PS5001; MCMPAL; 1.

R PROSITE; PS5001; MCMPAL; 1.

R PROSITE; PS5001; MCMPAL; 1.

R PROSITE; PS5001; MCMPAL; 1.

R PROSITE; PS5001; MCM 2; 1.

R SEQUENCE 1108 AA; 125967 MW; 92D2578B31351F75 CRC64;
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1108 AA; 125967 MW; 92D2578B31351F75 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1999 (TrEMBLrel. 09, Last sequence update)
01-OGN-2009 (TrEMBLrel. 25, Last annotation update)
1108AA long hypothetical cell division control protein.
                                                                                                                                                                                                                                               PRT; 1108 AA.
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                                         853 LSKIEHITPSAVRR 866
   . 1 MEKVQYLTRSAIRR 14
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RESULT 14 Q9UFE6

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Buthería; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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095213, PRELIMINARY; PRT; 1120 AA.
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OGT-2003 (TrEMBLrel. 25, Last annotation update)
Coiled-coil related protein DEEPEST (Mitotic spindle-associated protein p126).
                                                                                                                                                                                                                                                                                             Blum H., Bauersachs S., Mewes H.W., Cassenhuber J., Wiemann S.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AL122116; CABS-9275-1;
PIR; T34542, T34542,
PIR; T34542,
NON TER.
NON TER.
SEQÜENCE 452 Aa; 51951 MW; 05CEA84AF4A118FD CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment).
QUEEG,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Hypothetical protein (Fragment).
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Matches 10, Conservative
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Matches 10; Conservative
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                             SEQUENCE FROM N.A.
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           NCBI TaxID=9606;
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                                                           TISSUE=Lung
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SEQUENCE
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EMBL; AF399910; AAK91712.1; -. Genew; HGNC:13452; SPAG5.
SEQUENCE 1193 AA; 134383 MW; 174D3F563E9C4A8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21433483; PubMed=11549262;
MEDLINE=21433483; PubMed=11549262;
Ling M.C., Yang Y.C.,
Lin W.C., Yang Y.C.,
"Cloning and Characterization of hMAP126, a New Member of Mitotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Mitotic spindle coiled-coil related protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
             Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                            52.0%; Score 39.5; DB 4; Length 1120; 66.7%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                              Spindle-Associated Proteins.",
Blochem. Biophys. Res. Commun. 287:116-121(2001).
EMBL, AR003308, AAD02813.1; -.
EMBL, AF195347, AAL06396.1; -.
PIR; JC7765, JC7765.
SEQUENCE 1120 AA; 125683 NW; 3D01F7BA370F2645 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                        SEQUENCE FROM N.A.
Schnabel J., Weber K., Hatzfeld M.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-CT-2003 (TrEMBLrel. 25, Last ann
Mitotic spindle associated protein.
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1070 EEVTHLTRS-LRRAE 1083
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tes 10; Conservative
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DEEPEST
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polymorphisms.";

Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1996).

Broc. Natl. Acad. Sci. U.S.A. 0:0-0(1996).

GG 90:0016021; C:integral to membrane; IEA.

GG) GO:0019884; P:antigen presentation, exogenous antigen; IEA.

GG) GO:0019886; P:antigen presentation, exogenous antigen via M. .; IEA.

GG) GO:0019886; P:antigen presentation, exogenous antigen via M. .; IEA.

GG) GO:0019886; P:antigen presentation, exogenous antigen via M. .; IEA.

GG) GO:0019886; P:antigen presentation.

GG) GO:0019886; P:antigen presentation.

GG) GO:0019886; P:antigen presentation.

GG) GO:0019886; P:antigen presentation.

GG) GO:0019886; P:antigen presentation.

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GG) GO:0019886; P:antigen presentation.

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mamania, Butheria, Primates; Catarrhini, Cercopithecidae;
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                              1;
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"Ancestral MHC-DRB genes beget conserved patterns of localized
                                                                                                                                                                                                                Query Match 52.0%; Score 39.5; DB 4; Length 1193; Best Local Similarity 66.7%; Pred. No. 2.2e+02; Matches 10; Conservative 3; Mismatches 1; Indels 1;
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Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: BC000322; AAH00322.1; -.
SEQUENCE 1193 AA; 134421 MW; A846DBJFE624519C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 81
81 AA, 9700 MW, C372383CA3988F9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 01, Last sequence update) Major histocompatibility complex (Fragment). MANE-DRB6*PS01.
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last annotation update)
Transcriptional regulator.
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01-NOV-1996 (TrEMBLrel, 01, Last seq
01-JUN-2003 (TrEMBLrel, 24, Last anno
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Best Local Similarity 53.3.
Best & Conservative
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406 AA.

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MEDLINE-2243306; PubMed=12534463;
Melson K.E., Weihel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R. T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepndic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.3%; Score 39; DB 16; Length 406; 75.0%; Pred. No. 89; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4;799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein; Complete proteome.
406 AA; 47318 MW; 7CD8C30DF0D3C6E2 CRC64;
                                                                        01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TREMBLrel. 24, Last annotation update)
Hypothetical protein.
                      PRT;
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                                                                                                                                                                                                            Pseudomonas putida (strain KT2440).
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                         PRELIMINARY;
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Best Local Similarity
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Heilig R.;
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                                                                                                                                                                                              Fuji F., Hirama C., Nakamura I., Cywwww. A. Horikoshi K.;

Horikoshi K.;

"Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";

RL halodurans and genomic sequence comparison with Bacillus subtilis.";

RL Nucleic Acids Res. 28.4317-4331(2000).

CC -: SIMILARIYY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.

EMBL, APPONISIO; BAB04558.1; -.

DR GO; GO:000370; P: Firanscription factor activity; IEA.

CG: GO:000370; P: Firanscription of transcription, DNA-dependent; IEA.

DR GO; GO:0005355; P: Fequiation of transcription, DNA-dependent; IEA.

DR InterPro; IPR000847; HTH LysR.

DR Pfam; PF00126; HTH 1; 1.

Pfam; PF00126; HTH 1; 1.

DR Pfam; PF001466; LysR substrate; 1.

DR Pfam; PF00146; HTH LysR FAMILY; 1.

PROSTITE; PS00044; HTH LYSR FAMILY; 1.

DR PROSTITE; PS00044; HTH LYSR FAMILY; 1.

COMPLETE: PS00044; HTH LYSR FAMILY; 1.

COMPLETE: PS00044; HTH LYSR FAMILY; 1.

COMPLETE: PS00044; HTH LYSR FAMILY; 1.

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COMPLETE: PS00044; HTH LYSR FAMILY; 1.

COMPLETE: PS00044; HTH LYSR FAMILY; 1.
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STRAIN-SFROM N.A.

STRAIN-SFROM O / ATCC 700294 / Serotype M1;

MEDLINE-21192684; PubMed=11296296;

Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

Qlan Y., Jia H.G., Nadjar F.Z., Ren Q., Zhu H., Song L., White J.,

Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).

EMBL, AE006512; AAK33542.1;

EMBL, AD006512; AAK33542.1;

EMBL, AD006512; Complete proteome.

SEQUENCE 364 AA; 41754 MW; 038BBD36F4234020 CRC64;
                                                                                                                                                 MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                   Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein SPy0549.
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Best Local Similarity 46.7%
Then 7; Conservative
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Best Local Similarity 53.8³
Matches 7; Conservative
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                                                                                                     SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
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Bacillus halodurans
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Q9A0Y9; 09A0Y9 RESULT 21

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Gaps

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"Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248284; CAB49417.1;
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GO; GO:0005267; F:potassium channel activity; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPROJ622; K-channel_pore.
SEQUENCE 481 As, 55655 MW; 685FB30056A45259 CRC64;
                                                      01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 14, Last annotation update)
Hypotherical protein PYRAB04950.
481 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22559397; PubMed=12674476;
Kloetzel J.A., Barchetta S.,
Kloetzel J.A., Barchetta S.,
Farmar J., Banerte D., Fleury-Aubusson A.;
"Plateins: a novel family of signal peptide-containing articulins in euplotid cilates.";
"J. Enkaryot. Microbiol. 50:19-33(2003).
EMBL; AX124991; AAM94464.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

WhoMed=15615971;

Kloetzel J.A., Barrin-Tourancheau A., Miceli C., Barchetta S.,
Farmar J., Banerjee D., Pleury-Aubusson A.;

Farmar J., Banerjee D., Pleury-Aubusson A.;

Frankar J., Banerjee D., Pleury-Aubusson A.;

Frankar J., Banerjee D., Pleury-Aubusson A.;

Frankar J., Banerjee D., Pleury-Aubusson A.;

Frankar J., Barrin J., Pleury-Aubusson A.;

Frankar J., Barrin J., Barrin J., Barrin J., Barrin J., J., Cell Sci., 116:1291-1303 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLral. 25, Created)
01-OCT-2003 (TrEMBLral. 25, Last sequence update)
01-OCT-2003 (TrEMBLral. 25, Last annotation update)
01-OCT-2003 (TrEMBLral. 25, Last annotation update)
0SJNBA0008M17.1.
0SJNBA0008M17.1.
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
Euplotida; Euplotidae; Euplotes.
NCBI_TaxID=5940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.3%; Score 39; DB 5; Length 644; Best Local Similarity 54.5%; Pred. No. 1.5e+02; Matches 6; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7298E314EFB7417A CRC64;
                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                               644 AA
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2 EKVQYLTRSAIRRA 15
                      38 EKIKYIKRRAFERA 51
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DR EMBL; AL662950; CAD41786.1; -.

SQ SEQUENCE 688 AA; 76908 MW; CD8298225DB66523 CRC64;

Query Match

Best Local Similarity 66.7%; Pred. No. 1.6e+02;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps

Qy 5 QYLTRSAIRRAE 16

Db 562 QWVTRSARRTE 573

Search completed: October 1, 2004, 12:17:35
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

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Ade45177 Human SER
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Aag08266 Arabidops Abu29277 Protein e

ALIGNMENTS

AAY71009 standard; peptide; 16 AA.

AAY71009;

(first entry) 29-AUG-2000 Human Phospholamban (PLB) cargo peptide.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATFase; SERCA2a; cardiant, cardiamycorpe; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; mycoardial dysfunction.

Homo sapiens.

WO200025804-A2.

11-MAY-2000.

99WO-US025692. 02-NOV-1999;

02-NOV-1998; 27-JUL-1999;

98US-0106718P. 99US-0145883P.

(REGC ) UNIV CALIFORNIA.

не н, Minamisawa S, Dillman W, Chien K, Scott C,

Silverman GJ;

Wang Y,

Hoshijima M, Meyer M;

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase

Example 4; Page 50; 56pp; English.

small peptide complexes and recombinat proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum C2 + Arbase (SERCA2A) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractility). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the cargo peptide from human PLB aminot terminal residues 1-16. It could be derived from any segment of wild type or mutant PLB protein. The cargo peptide is linked to the transport peptide by a covalent linkage The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces 

Sequence 16 AA;

Gaps ò / Match 100.0%; Score 75; DB 3; Length 16; Local Similarity 100.0%; Pred. No. 1e-06; les 16; Conservative 0; Mismatches 0; Indels Query Match Best Loca Matches

Š

AAY71012 standard; peptide; 35 AA. RESULT 2 AAY7101

AAY71012;

(first entry) 29-AUG-2000

Penetratin-based recombinant phospholamban peptide, TAT-PLB.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiamyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; recombinant peptide; HIV; TAT protein.

Human immunodeficiency virus. Homo sapiens

Location/Qualifiers

Region

5. 15 /note= "Corresponds to denatured human immunodeficiency virus (HIV) TAT protein"

.35

Region

/note= "Corresponds to human phospholamban (PLB) amino terminal peptide"

WO200025804-A2.

11-MAY-2000.

02-NOV-1999;

02-NOV-1998;

98US-0106718P. 99US-0145883P. 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

Chien K, Dillman W, Minamisawa S, Scott C, Wang Y, Silverman GJ;

Meyer M;

Hoshijima M,

не н,

WPI; 2000-365393/31.

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase. 

Example 5; Page 52; 56pp; English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum (as 4 + AFpase (SERCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargot peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractiin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinant protein, attached to the 3' end of denatured human immunodeficiency virus (HIV), TAT protein. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the plasma membrane

Sequence 35 AA;

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; 0 100.0%; Score 75; DB 3; Length 35; 100.0%; Pred. No. 2.4e-06; Indels 100.0%; Prec. No. -Conservative Best Local Similarity Matches 16; Conserv Query Match

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Gaps

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Phospholamban; PLB; human, sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiamt; cardiomyocyte; transport peptide; penetratin; cardio cardiomyocyte; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; recombinant peptide; fruit fly; antennapedia; ANT.
                                                                                                                                                                                                   1. 20
/note= "Corresponds to human phospholamban (PLB) amino
terminal peptide"

    .36
/note= "Corresponds to Drosophila antennapedia (ANT)
transport peptide"

                                                                                                    Penetratin-based recombinant phospholamban peptide, PLB-ANT.
                                                                                                                                                                                           Location/Qualifiers
                                                     AAY71011 standard; peptide; 36 AA
1 MEKVOYLTRSAIRRAS 16
           MEKVQYLTRSAIRRAS
                                                                                    (first entry)
                                                                                                                                                                                                                                                         WO200025804-A2
                                                                                                                                                                           Drosophila sp.
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                                      RESULT 3
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H, Hoshijima M, Meyer M; He Dillman W, Minamisawa S, Wang Y, Silverman GJ; 98US-0106718P. 99US-0145883P. 99WO-US025692. (REGC ) UNIV CALIFORNIA. Chien K, Scott C,

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase

WPI; 2000-365393/31

Example 5; Page 52; 56pp; English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPase (BERCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myccardial for the gysfunction. The present sequence is the penetratin-based recombinant peptide PLB-MT, comprising the amino terminal end of human PLB native protein, attached to the 5' end of the Drosophila antennapedia (ANT) cansport peptide. Penetratin is a class of peptides, with translocating processing and manner and mycrafile PLB-MT, can also not be protein, a class of peptides, with translocating a passed across the olasma membrane

Seguence 36 AA;

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                                                                                                                                        Human, SERCA 2, phospholamban, PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum, protein co-ordinate data,
cardiant.
                     Gaps
                     .;
       Length 36;
Score 75; DB 3; Lengtn 30, Pred, No. 2.5e-06;
                                                                                                                                                                                                                                                       M, Tenhunen J, Vidgren J;
Tilgmann C, Lotta T, Kaivola J;
                                                                                                                          Human SERCA_2 inhibitor phospholamban, cytosolic domain.
                                                                                ADE45175 standard, peptide, 36 AA.
                   ;
0
      th 100.0%;
| Similarity 100.0%;
| 16; Conservative 0
                                                                                                                                                                                                              99US-00252063.
                                              16
                                1 MEKVOYLTRSAIRRAS 16
                                                                                                                                                                                                                            97US-00937117.
                                              1 MEKVQYLTRSAIRRAS
                                                                                                            29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                        Ovaska M,
                                                                                                                                                                                                                                                              Yliperttula-Ikonen M,
                                                                                                                                                                                                                                                                           WPI; 2004-019625/02.
    Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                        (ORIN ) ORION CORP.
                                                                                                                                                                                                                                                      Pollesello P,
                                                                                                                                                                                                              18-FEB-1999;
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                 US6538022-B1
                                                                                                                                                                                                25-MAR-2003.
                                                                                               ADE45175;
                                                                   RESULT 4
                                                                          ADE45175
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                                             Ωp
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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, 224 ArPase of the sarco/endoplasmic reticulum, appearing as ADB45167-ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site comprises ATS-14; a hydrophobic moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzopyzan-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the compound is refected a phospholamban on cardiac SERCA-2. The present sequence is the effects of phospholamban on cardiac SERCA-2. The present sequence is the

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATFase by deactivating phospholamban and stimulating Ca2+

Disclosure, SEQ ID NO 9, 65pp, English.

-ATPase.

Sequence 36 AA;

ö Gaps ; 0 Length 36; 100.0%; Score 75; DB 8; Length 36 larity 100.0%; Pred. No. 2.5e-06; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 16; Conserv

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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum C2 + ATPase (SERA2a) within cardiomyocytes. The peptide scomplex comprises of transport peptide like penetratin and cargo peptide complex comprises of transport peptide like penetratin and PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g., heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising a sense mutation Val49Ala. This mutant sequence when contractility than the wild type PLB sequence.
                                                                                                                                                                                                                                                     Phospholamban, PLB, human; sarcoplasmic reticulum Ca 2+ ATPase, SERCA2a, cardiant, cardiomycoyte, transport peptide, penetratin, cargo peptide, contractility, inhibitor, cardiac disease, treatment; heart failure; mycoardial dysfunction; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 75; DB 3; Length 52; 100.0%; Pred. No. 3.7e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Val replaced with Ala"
                                                                                                                                                                                                                     Human mutant phospholamban (PLB) V49A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minamisawa S,
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 48; 56pp; English.
                                                                                                                   AAY71003 standard; protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang Y, Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US025692.
16
                    1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0106718P
1 MEKVOYLTRSAIRRAS
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-365393/31.
                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200025804-A2
                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 - JUL-1999;
                                                                                                                                                                                     29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-2000.
                                                                                                                                                    AAY71003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chien K,
Scott C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                    AAY71003
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98US-0106718P.
99US-0145883P.
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1 MEKVOYLTRSAIRRAS 16
                                                                                                                                 29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-365393/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200025804-A2.
                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-2000.
                                                                                                       AAY71002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chien K,
Scott C,
                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                Key
                                                    RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   He H, Hoshijima M, Meyer M;
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small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ Arrest (SERCA2a) within cattorn between PLB and sarcoplasmic reticulum Ca 2+ Arrestor (SERCA2a) within cattorn between PLB respected complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac confractility and reduces blood pressure. This method is useful for the dysfunction. The present amino acid sequence is the human PLB wild type protein, a potent inhibitor of SERCA2a acidivity. It primarily exists in a pentameric form. It is a mediator in the regulation of myocardial function by catecholamines through the cAMP cascade
                                                                                                                                       Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomycoytre; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Domain_II
/note= "Transmembrane sector made of uncharged residues
responsible for stabilising the pentamer formation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The patent discloses a method for the treatment of heart failure, using
                                                                                                                                                                                                                                                                                   1. .20
/label= Domain Ia
/note= "Rich in alpha-helical confirmation with a net
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meyer M;
                                                                                                                                                                                                                                                                                                                                                    /label= Domain_Ib
/note= "Cytoplasmic sector of the monomer"
31. .52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoshijima M,
                                                                                                       Human Phospholamban (PLB) wild type protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 He
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minamisawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 47; 56pp; English.
AAY71002 standard; protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                      positive charge"
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Sequence 52 AA;

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Gaps

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1 MEKVQYLTRSAIRRAS 16

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Local Similarity 100.

Best Loca Matches

reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did no form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pot\_sequences

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Gaps

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0; Indels

Score 75; DB 5; I Pred. No. 3.7e-06; Mismatches

100.08; F. 100.08;

Query Match
Best Local Similarity 100.
Matches 16; Conservative

Sequence 52 AA;

8X33333

1 MEKVQYLTRSAIRRAS 16

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0;
                                                                                                                                                                              Human; open reading frame; OREX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; ostecarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                      Gaps
                      .
0
 100.0%; Score 75; DB 3; Length 52; 100.0%; Pred. No. 3.7e-06;
                    Indels
                     ;
0
                                                                                                                                                             Human ORFX protein sequence SEQ ID NO:13166.
                    Mismatches
                                                                                                        AA.
                    .
                                                                                                    ABP06592 standard; protein; 52
                                     1 MEKVOYLTRSAIRRAS 16
                                                      1 MEKVOYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                           29-MAY-2001; 2001WO-US010836.
                                                                                                                                           (first entry)
        Similarity 100.
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                  myasthenia gravis.
                                                                                                                                                                                                                                                                                     WO200192523-A2,
                                                                                                                                                                                                                                                                     Homo sapiens.
Query Match
Best Local Simi
Matches 16;
                                                                                                                                           25-JUN-2002
                                                                                                                                                                                                                                                                                                          06-DEC-2001
                                                                                                                       ABP06592;
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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, Ca2+ ArPase of the sarco/endoplasmic reticulum) appearing as ADB45167-ADB45167-ADB45167. The compound has a structure containing three of the four of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises TYT-6. Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site comprises Arg-14; a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is not 3-berayl-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is not 3-berayl-57-bis ([H-tetrazol-5-y1)-methyloxy)-4-methyl-2H-1-benzopyran-2-one Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the CA2 + -ATPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                                                                                         Mouse; SERCA_2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pound, useful for relieving inhibitory effects of phospholamban on SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovaska M, Tenhunen J, Vidgren J_j onen M, Tilgmann C, Lotta T, Kaivola J_j
                                                                                                                                                                                                                    Mouse SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 6; 65pp; English.
                                                                                                   ADE45172 standard; protein; 52 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00252063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-00937117.
  1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                              29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pollesello P, Ovaska
Yliperttula-Ikonen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-019625/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORIN ) ORION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compound,
                                                                                                                                                                                                                                                                                                                                                                              US6538022-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1997;
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                                                                                                                                         ADE45172;
                                                                                                                                                                                                                                                                                               cardiant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATPase.
                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                               ADE45172
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 or the the specification). ABN15762 to ABN27552 encode the human ORFX proteins are useful for proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide syndrome associated with ORFX-associated disorders. Associated on the careful of the following of the cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benjud undurs, kaloid, degenerative disorders haemorrhage, of treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benjud undurs, kaloid, degenerative disorders haemorrhage, transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders mellitus, systemic storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also bone degenerative disorders, incisions, ulcers, for treating osteoprosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,

Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

Shimkets RA, Leach MD;

WPI; 2002-106308/14. N-PSDB; ABN22344.

Disclosure; SEQ ID NO 13166; 1037pp; English.

100.0%;

Best Local Similarity

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The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, 22.4 ATPage of the sarco/endoplasmic reticulum ) appearing as ADB45167-ADB4513. The compound has a tructure containing three of the four moietises; an electromegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electromegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound. the S2 binding site of the phospholamban cytosolic comain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-21, 22 and/or Phospholamban, comprising administering the included are deactivating phospholamban, comprising administering the involvence is a compound is a useful for relieving the inhibitory effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rabbit; SERCA 2, phospholamban; PLB; Ca2+ Afpase o\(\bar{t}\) the sarco/endoplasmic reticulum; protein co-ordinate data; cardiant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                                               Length 52;
                                                                            Query Match 100.0%; Score 75; DB 8; Length 52 Best Local Similarity 100.0%; Pred. No. 3.7e-06; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovaska M, Tenhunen J, Vidgren J;
onen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabbit SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 4; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  ADE45170 standard; protein; 52 AA.
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                                                                                                                                                                                          1 MEKVOYLTRSAIRRAS 16
                                                                                                                                                                                                                                            1 MEKVOYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pollesello P, Ovaska
Yliperttula-Ikonen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-019625/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ORIN ) ORION CORP.
                          Sequence 52 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6538022-B1.
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XX SS
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100.0%; Score 75; DB 8; Length 52;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an 81 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain associating with an S4 binding site of the phospholamban cytosolic domain
                                                                                                                                                                                                                                                                                                                                             Rat; SERCA_2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      when the compound is bound, the binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzyl-5,7-bis (lH-tetrazol-5-yl)-methyloxy)-4-methyl.2H-lbenzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2 + -APPase. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                    Gaps
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                  Indels
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onen M, Tilgmann C, Lotta T, Kaivola J;
Pred. No. 3.7e-06; Mismatches 0;
                  0; Mismatches
                                                                                                                                                                                                                                                                                                          Rat SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 5; 65pp; English.
                                                                                                                                                                                            ADE45171 standard; protein; 52 AA.
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                                                       1 MEKVOYLTRSAIRRAS 16
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                                                                              1 MEKVQYLTRSAIRRAS
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Best Local Similarity 100.0
Matches 16; Conservative
                    16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-019625/02.
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                    Matches
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ADE45167 RESULT

ADE45167 standard; protein; 52

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ADE45167;

(first entry) 29-JAN-2004 Human SERCA\_2 inhibitor phospholamban,

1; SERCA\_2; phospholamban; PLB; ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data; cardiant.

Homo sapiens

Location/Qualifiers Key Binding-site

note= "S1 binding site residue claimed in claim 1" note= Binding-site Binding-site

note= Binding-site

"S1 binding site residue claimed in claim 1" "S1 binding site residue claimed

in claim 1" claim 1" in claim 1" i.n binding site residue claimed residue note= "S2 binding site ... 83 note= Binding-site Binding-site

in claim 1" in claim 1" "S4 binding site residue claimed in claim 1" "S3 binding site residue claimed "S3 binding site residue claimed note= note= note= Binding-site Binding-site Binding-site

"S4 binding site residue claimed in claim 1"

US6538022-B1

25-MAR-2003

99US-00252063, 18-FEB-1999;

97US-00937117 24-SEP-1997;

(ORIN ) ORION CORP.

Tenhunen J, Vidgren J; lamann C, Lotta T, Kaivola J; Ovaska M, Tennam. Yliperttula-Ikonen M, Pollesello P,

WPI; 2004-019625/02

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+ -ATPase.

WO200025804-A2

11-MAY-2000

Claim 1; SEQ ID NO 1; 65pp; English.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA\_2, Ca2+ ATPEASIOF. The sarcof-endoplasmer reticulum?) appearing as ADE45167-ADE45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an SI binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyre, ATG-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic Arg-14; a hydrophobic moiety associating with an S3 binding site comprises phospholamban cytosolic domain when the compound to it, the S2 binding site comprises phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic moiety 

associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzyls.7-bis (IH-tetrazol-5-yl)-methyloxy)-4-methyl-2H-methyl-2H-1-benzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca. 4-ATPRESE. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA\_2. The present sequence is Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine. /note= "Corresponds to mutant human phospholamban (PLB) H6 tagged penetratin-based recombinant protein, H6-(V49A)mutantPLB-ANT. Gaps /note= "Corresponds to Drosophila antennapedia (ANT) transport peptide" .. Indels .58 :e= "Corresponds to hexahistidine tag "Wild type Val replaced with Ala" Length 100.0%; Score 75; DB 8; I 100.0%; Pred. No. 3.7e-06; ive 0; Mismatches 0; Location/Qualifiers AAY71019 standard; protein; 79 AA. 1 MEKVOYLTRSAIRRAS 16 16 1 MEKVQYLTRSAIRRAS (first entry) 16; Conservative protein" 63. .78 /note= "C note= /note= Local Similarity Sequence 52 AA; Misc-difference Drosophila sp. Synthetic. sapiens 29-AUG-2000 AAY71019; Query Match Key Region Region Region Matches RESULT 12 Ношо AAY71019 8888888888 à 셤

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Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine Σ. Meyer Hoshijima M, He H, Minamisawa S, Silverman GJ; 98US-0106718P. 99US-0145883P. 99WO-US025692 (REGC ) UNIV CALIFORNIA. Dillman W, WPI; 2000-365393/31. Wang 02-NOV-1999; 27-JUL-1999; 32-NOV-1998; Chien K, Scott C,

triphosphatase

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small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum (2 + Arpase (SERCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and carcop peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and mycoardial dysfunction. The present sequence is the hexahistidine (H6) tagged penetratin-based recombinant protein H6-mutantPLB-ANT, comprising the turnsport peptide attached by a hexahistidine tag. This sequence is expressed in Escherichia coli cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Corresponds to Human phospholamban (PLB) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a, cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; H6 tag; hexahistidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hexahistidine tagged penetratin-based recombinant protein, H6-wtPLB-ANT.
                  The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinate controls.
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/note= "Corresponds to Drosophila antennapedia (ANT)
transport peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Corresponds to hexahistidine tag (H6)"
                                                                                                                                                                                                                                                                                                                                       100.0%; Score 75; DB 3; Length 79; 100.0%; Pred. No. 5.8e-06;
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Wang Y, Silverman GJ;
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Example 6; Page 56; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71017 standard; protein; 79 AA.
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99US-0145883P.
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                                                                                                                                                                                                                                                                                                        Sequence 79 AA;
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Synthetic.
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Scott C,
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small peptide complexes and recombinant protectins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ Arpase (SERCAZa) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as a dominant negative inhibitor of FLB-SERCAZa interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the hexahistidine (H6) tagged penetratin-based recombinant protein H6-wtPLB-ANT, comprising the wild type human PLB protein and brosophila antennapedia (ANT) transport Escherichia coli cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant.
           Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                  patent discloses a method for the treatment of heart failure, using
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                                                                                                 Example 6; Page 54-55; 56pp; English.
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Wang Y, Silverman GJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY71006 standard; protein; 52 AA.
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99US-0145883P.
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 79 AA;
                                                                    triphosphatase.
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Scott C,
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Gaps

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Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                             triphosphatase.
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Disclosure, Page 49, 56pp, English.

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (FLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum C2 + ArPase (SERCA2a) within cardiomycyptes. The peptide selected from mutant PLB, native FLB or antibody against PLB protein (contractilin). Penetratin-FLB peptide functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the mutation Serl6Ann. This mutant sequence when overexpressed in the transformed cardiomycoytes, shows increased contractility than the wild type PLB sequence 

Sequence 52 AA;

Gaps . 0 96.0%; Score 72; DB 3; Length 52; 93.8%; Pred. No. 1.3e-05; tive 1; Mismatches 0; Indels 1 MEKVQYLTRSAIRRAS 16 1 MEKVOYLTRSAIRRAN 16 Conservative Local Similarity es 15; Conserv Query Match Matches g

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ADE45168 standard; protein; 52 AA. ADE45168

ADE45168; 

29-JAN-2004 (first entry)

Pig SERCA\_2 inhibitor phospholamban.

ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data; Pig; SERCA\_2; phospholamban; PLB; Ca2+ ATPase of the sarco/endonlasm cardiant

Sus sp.

US6538022-B1

25-MAR-2003

99US-00252063. 18-FEB-1999; 97US-00937117. 24-SEP-1997;

(ORIN ) ORION CORP.

Pollesello P, Ovaska M, Tenhunen J, Vidgren J; Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J; WPI; 2004-019625/02.

New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+

Claim 1; SEQ ID NO 2; 65pp; English.

-ATPase.

The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, Ca2+ ATPase of the sarco/endoplasmic reticulum ) appearing as ADE45167-

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ADB45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr.6, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is not 3-benzyl-5/-bis ([H+tetrazol-5-y]) methyloxy) 4 methyl-2H-methyl-2H-methyl-2H-methyloxyl-4-compound is not 3-benzyl-5/-bis ([H-tetrazol-5-y]) methyloxyl-4-compound is not 3-benzyl-sing the involed are deactivating the case the Ca 2 + -ATPase. The compound is useful for relieving the inhibitory and the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the cas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dog; SERCA 2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 96.0%; Score 72; DB 8; Length 52; Best Local Similarity 93.8%; Pred. No. 1.3e-05; Matches 15; Conservative 1; Mismatches 0; Indels
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onen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 3; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dog SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE45169 standard; protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00252063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00937117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-019625/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ORIN ) ORION CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pollesello P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16
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molety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site comprises pag-14; a hydrophobic molety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-28; and a hydrophobic molety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site of the phospholamban cytosolic domain when the compound is not 3-benzoyxan-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2 + ATPsas. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phospholamban, PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a, cardiant, cardiachemycorpte; transport peptide; penetratin, cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Corresponds to denatured human immunodeficiency virus (HIV) TAT protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Corresponds to mutant human phospholamban (PLB) amino terminal peptide"
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penetratin-based recombinant phospholamban peptide, TAT-mutant PLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minamisawa S, He H, Hoshijima M, Meyer M;
                                                                                                                                                                                                                                                                                                 Query Match 96.0%; Score 72; DB 8; Length 52; Best Local Similarity 93.8%; Pred. No. 1.3e-05; Matches 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild type Ser replaced with Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY71014 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                            1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                              1 MDKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US025692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16. .35
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Scott C, Wang Y, Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; TAT protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200025804-A2
                                                                                                                                                                                                                              phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
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mall peptide complexes and recombinant proteins, that induces phospholamban (FLB) deficiency and inhibits the interaction between PLB and sarcoplasmic retuciun (a 2 + ATPase (SERCA2A) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide complex comprises of transport peptide like penetratin and protein (contractilin). Penetratin-PLB peptide like penetratin and of minant negative inhibitor of PLB-SERCA2 interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial contractility comprising the amino terminal end of human PLB mutant PLB, comprising the amino terminal end of human PLB mutant (Seriallu) protein, attached to the 3' end of denatured human communodeficiency virus (HIV), TAT protein. Penetratin is a class of phydrophilic compounds across the plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiant; cardiomycyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility, inhibitor; cardiac disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a;
                                                                  The patent discloses a method for the treatment of heart failure, using

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/note= "Corresponds to mutant human phospholamban (PLB)
amino terminal peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penetratin-based recombinant phospholamban peptide, mutant PLB-ANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meyer M;
                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                          94.7%; Score 71; DB 3; Length 35; 100.0%; Pred. No. 1.3e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoshijima M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Wild type Ser replaced with Glu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chien K, Dillman W, Minamisawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                               Example 5; Page 53; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71013 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0106718P.
99US-0145883P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fruit fly; ANT; antennapedia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 MEKVOYLTRSAIRRA 30
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                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                             Sequence 35 AA;
triphosphatase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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AAY71013
ID AAY71
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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ APPase (SERCAZa) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against Complex complex complex compressed in the peptide functions as a cominant negative inhibitor of PLB-SERCAZa interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the penetratin-based recombinant peptide, mutant PLB-ANT, comprising the amino terminal end of human PLB mutant (SeriGGlu) proteath, attached to the 5' end of the Drosophila antennapedia (ANT) transport peptide. Penetratin is a class of peptides, with translocating properties having the ability to carry hydrophilic compounds across the plasma membrane
                                                                Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; phospholamban; PLB; cardiant; heart disease; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.7%; Score 71; DB 3; Length 36; 100.0%; Pred. No. 1.3e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human phospholamban pseudophosphorylation mutant S16E PLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wildtype Ser substituted by Glu"
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                                                                                                                                                  Example 5; Page 53; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB79404 standard; peptide; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiac function; mutant; mutein.
 Wang Y, Silverman GJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-2001; 2001US-00954571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEKVOYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.'
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoshijma M,
                                WPI; 2000-365393/31.
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IKEDA Y.
                                                                                                                  triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 AA;
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 Scott C,
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                              Delivering a dose of a gene expression cassette in a fluid selectively to heart for sustained expression, useful for improving or enhancing cardiac function, by employing a viral vector together with a vascular
                                                                                                                                   The invention relates to delivering a therapeutic dose of a gene expression cassette in a fluid selectively to heart for sustained expression, comprising employing a viral vector together with a vascular permeabilising agent. The method is useful for gene therapy delivering genes for improving or enhancing cardiac function, particularly in passet of heart disease. The present sequence is that of a pseudophosphorylation mutant of phospholamban (SiGEPLB). This point mutant is among a number of dominant negative mutants identified and characterised in WO00/25804 and used in the method of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken; SERCA_2; phospholamban; PLB;
Ca2+ ATPase of the sarco/endoplasmic reticulum; protein co-ordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compound, useful for relieving inhibitory effects of phospholamban on cardiac SR Ca2+-ATPase by deactivating phospholamban and stimulating Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a compound which deactivates, and exhibits affinity for, a phospholamban (PLB) protein (an inhibitor of SERCA 2, Ca2+ ATFase of the sarco/endoplasmic reticulum ) appearing as ADB45167-ADB45173. The compound has a structure containing three of the four moieties: an electronegative moiety associating with an S1 binding site
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 2e-05;
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Yliperttula-Ikonen M, Tilgmann C, Lotta T, Kaivola J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken SERCA_2 inhibitor phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 7; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE45173 standard; protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                     94.7%; Scor.
100.0%; Pre
                                                                                                          Example 6; Fig 1; 12pp; English.
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Best Local Similarity 100.
Matches 15; Conservative
 WPI; 2002-361185/39.
                                                                           permeablizing agent
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                                                                                                                                                                                                                                                                                                                 Sequence 52 AA;
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                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus sp.
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of the phospholamban cytosolic domain when the compound is bound to it, the binding site comprises Tyr-6, Arg-9 and/or Arg-13; an electronegative moiety associating with an S2 binding site of the phospholamban cytosolic domain when the compound is bound to it, the S2 binding site comprises Arg-14; a hydrophobic moiety associating with an S3 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Met-20, Lys-27 and/or Leu-38; and a hydrophobic moiety associating with an S4 binding site of the phospholamban cytosolic domain when the compound is bound, the binding site comprises Phe-32 and/or Phe-35. The compound is not 3-benzopyran-2-one. Also included are deactivating phospholamban, comprising administering the novel compound to stimulate the Ca 2 + -ATPass. The compound is useful for relieving the inhibitory effects of phospholamban on cardiac SERCA_2. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATFase; SERCAZa; cardiant; cardiomyocyte; transport peptide; penetratin; cardia cardiae contractility; inhibitor; cardiae disease; mutant; treatment; heart failure; myocardial dysfunction; recombinant protein; fruit fly; ANT; antennapedia; He tag; hexahistidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H6 tagged penetratin-based recombinant protein, H6-(S16E)mutantPLB-ANT.
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                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Corresponds to Drosophila antennapedia (ANT) transport peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53. .58
/note= "Corresponds to hexahistidine tag (H6)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY71018 standard; protein; 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                  1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                    1 MEKVQYITRSALRRAS 16
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                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                              Sequence 52 AA;
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Drosophila sp.
Synthetic.
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                                                                                                                                                                                                                                               phospholamban.
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Scott C,
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The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ ATPsea (SERCA2A) within cardiomycytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PLB, native PLB or antibody against PLB protein (contractilin). Penetratin-PLB peptide functions as dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present sequence is the hexahistidine (HS) tagged penetratin-based recombinant protein H6-matantPLB-NNT, comprising the human mutant (SerlGGlu) PLB protein and Drosophila antennapedia (ANT) transport peptide attached by a hexahistidine tag. This sequence is expressed in Bscherichia coli cells
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                                                       Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild type Arg replaced with Glu"
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Wang Y, Silverman GJ;
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                                                                                                                                                                                                                                        Example 6; Page 55; 56pp; English.
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99US-0145883P.
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Matches 15; Conservative
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                                                                                                                                                                         triphosphatase.
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Scott C,
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WPI; 2000-365393/31.

small peptide complexes and recombinant proteins, that induces thospholamban (PLB) deficiency and inhibits the interaction between PLB and sarcoplasmic reticulum Ca 2+ Arpase (SERCASa) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide complex comprises of transport peptide like penetratin and the preptide selected from mutant PLB, native PLB or antibody against dominant negative inhibitor of PLB-SERCASa interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising a sense mutanion Argiddlu. This mutant sequence when overexpressed in the transformed cardiomycoytes, shows increased contractility than the wild type PLB sequence Treating cardiac diseases, e.g. heart failure or myocardial dysfunction comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase. The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant controls. Disclosure; Page 48-49; 56pp; English.

Sequence 52 AA;

93.3%; Score 70; DB 3; Length 52; 93.8%; Pred. No. 3e-05; 1; Indels Mismatches . 1 MEKVOYLTRSAIRRAS 16 1 MEKVQYLTRSAIREAS 16 Conservative Query Match Best Local Similarity Matches 15; Conserv 8 g

AAY71004 standard; protein; 52 AA AAY71004;

(first entry) 29-AUG-2000

Human mutant phospholamban (PLB) E2A protein.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant. RESULT 2:
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Synthetic.

Location/Qualifiers Misc-difference

/note= "Wild type Glu replaced with Ala"

WO200025804-A2

11-MAY-2000.

99WO-US025692 02-NOV-1999;

98US-0106718P 99US-0145883P. 02-NOV-1998; 27-JUL-1999;

(REGC ) UNIV CALIFORNIA.

Hoshijima M, Ä He ŝ Dillman W, Minamisawa Wang Y, Silverman GJ; Dillman W, Chien K, Scott C,

WPI; 2000-365393/31

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PIB) deficiency and inhibits the interaction between PIB and sarcoplasmic reticulum Ca 2+ ATPase (SBRCA2a) within cardiomycoytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutant PIB, native PIB or antibody against PIB protein (contractility). Penetratin-PIB peptide functions as a contractility and reduces blood pressure. This method is useful for the treatment of cardiac disease e.g. heart failure and myocardial dysfunction. The present amino acid sequence is the human mutant PIB protein, comprising the mutation Glu2Ala. This mutant sequence when overexpressed in the transformed cardiomycoytes, shows increased contractility than the wild type PIB sequence. se enhancing cardiac contractility by inhibiting interaction phospholamban and sarcoplasmic reticulum calcium 2+ adenosine English. 48; 56pp; Disclosure; Page triphosphatase small re comprises ( 

Sequence 52 AA;

Gaps ö Length 52; 1; Indels 92.0%; Score 69; DB 3; I 93.8%; Pred. No. 4.6e-05; 0; Mismatches Query Match Best Local Similarity 93.89 Watches 15; Conservative

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1 MEKVQYLTRSAIRRAS 16 1 MAKVOYLTRSAIRRAS

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Gaps . 0

RESULT 24

Š AAY71007 standard, protein, 52

AAY71007;

29-AUG-2000 (first entry)

Human mutant phospholamban (PLB) K3E/R14E protein.

Phospholamban; PLB; human; sarcoplasmic reticulum Ca 2+ ATPase; SERCA2a; cardiant; cardiomyocyte; transport peptide; penetratin; cargo peptide; contractilin; cardiac contractility; inhibitor; cardiac disease; treatment; heart failure; myocardial dysfunction; mutant. 

Homo sapiens. Synthetic.

note= "Wild type Lys replaced with Glu" Location/Qualifiers Key Misc-difference

/note= "Wild type Arg replaced with Glu" Misc-difference

WO200025804-A2

11-MAY-2000

02-NOV-1999;

98US-0106718P. 99US-0145883P. 27-JUL-1999; 02-NOV-1998;

(REGC ) UNIV CALIFORNIA.

Meyer Hoshijima M, не н, ω Dillman W, Minamisawa Silverman GJ; Wang Y, κ, r, Chien Scott

WPI; 2000-365393/31

Treating cardiac diseases, e.g. heart failure or myocardial dysfunction

comprises enhancing cardiac contractility by inhibiting interaction between phospholamban and sarcoplasmic reticulum calcium 2+ adenosine triphosphatase.

Disclosure; Page 49; 56pp; English

The patent discloses a method for the treatment of heart failure, using small peptide complexes and recombinant proteins, that induces phospholamban (PLD) deficiency and inhibits the interaction between PLB carcophasmic reticulum Ca 2+ Arpase (SERCA2a) within cardiomyocytes. The peptide complex comprises of transport peptide like penetratin and cargo peptide selected from mutent PLB, native PLB or antibody against cargo peptide selected from mutent PLB pertiae functions as a dominant negative inhibitor of PLB-SERCA2a interaction, enhances cardiac contractility and reduces blood pressure. This method is useful for the contractility and reduces blood pressure. This method is useful for the dysfunction. The present amino acid sequence is the human mutant PLB protein, comprising the double mutantion Lyssilu and ArgisGlu. This mutant sequence, when overexpressed in the transformed cardiomycoytes, shows increased contractility than the wild type PLB sequence mutant cardiac

Sequence 52 AA;

ö Gabs ö Length 52; 1; Indels 88.0%; Score 66; DB 3; I 87.5%; Pred. No. 0.00016; ive 1; Mismatches 1; Conservative Query Match Best Local Similarity Matches 14; Conserv

1 MEKVQYLTRSAIRRAS 16

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1 MEEVQYLTRSAIREAS 16

RESULT 25

ADC87928 standard; protein; 116 AA. ADC87928 CXSXTTXEXEXEXEXEXEXEXEXEXEXEXEXEXEXEX

ADC87928;

Ribosomal protein similar to FCWP1 #144.

(first entry)

01-JAN-2004

Antifungal protein; ribosomal protein; FCWPI; AlyAFP; plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora; Colletotrichum; Diplodia; Fusarium; Gaeumanomyces; Helminthosporium; Macrophomina; Myosphaerella; Nectria; Peronospora; Phomespora; Phomespora; Phomespora; Phomespora; Phomespora; Phomespora; Pyricularia; Pythium; Rhizoctonia; Scerotium; Sclerotinia; Septoria; Thielaviopsis; Venturia; Verticillium.

Unidentified

US6573361-B1

03-JUN-2003.

07-DEC-2000; 2000US-00732210.

99US-0169340P. 99US-0169513P. 07-DEC-1999; 07-DEC-1999; (MONS ) MONSANTO TECHNOLOGY LLC.

YS; ΜĽ Seale JW, Mittanck CA, Liang J, Bunkers GJ,

WPI; 2003-754558/71.

Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful for controlling fungal infections in plants. Example 21; SEQ ID NO 181; 27pp; English.

The invention relates to an isolated antifungal ribosomal protein from

cuerdul for controlling fungal infections in plants, such as the controlling fungal infections in plants, such as the controlling fungal infections in plants, such as the cockyta (e.g. Alcernaria brassicola, Alternaria cinerea), accoragora celegations at kinchii, cercospora zeae-maydis), cercospora zeae-maydis), cercospora zeae-maydis), collectrichum (e.g. Collectrichum lindemuthianum), Diplodia (e.g. Collectrichum (e.g. Fusarium nivale, Fusarium avysporum, planting paranium roseum), Rusarium culmorum, Fusarium solani, Fusarium compliceme, Fusarium carbonum, Helminthosporium maydis), Macrophomina cheminic paraniparium phaseolina, Meditia (e.g. Helminthosporium maydis), Macrophomina (e.g. Mycosphaerella figiensis), Nectria (Nectria Macrophomina (e.g. Mycosphaerella figiensis), Nectria (Nectria branatococca), Phoma betee ), Phyradetrichum (e.g. Phymatotrichum omnivorum), Phyrophthora (e.g. Phyrophthora cinnamoni, Phyrophthora capacina), Phyrophthora capacina, Phyrophthora and baseoli, Phyrophthora cinnamoni, Phyrophthora (e.g. Phyrophthora cinnamoni, Phyrophthora (e.g. Phyrophthora cinnamoni, Phyrophthora (e.g. Phyrophthora cinnamoni, Phyrophthora (e.g. Phyrophthora cinnamoni, Phyrophthora (e.g. Phyrophthora cinnamoni, Phyrophthora (e.g. Phyrophthora cinnamoni, Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrophthora (e.g. Phyrop signal peptide of the antifungal protein AlyAFP from Alyssum and FCWP1, encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are useful for controlling fungal infections in plants, such as those caused antifungal proteins. The present sequence represents one of the riboson proteins similar to FCWP1. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in fusarium culmorum, FCWP1. Also included is a fusion protein between electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6573361B1 

Sequence 116 AA;

ö Gaps ő 54.7%; Score 41; DB 7; Length 116; 46.7%; Pred. No. 14; 3; Indels ive 5; Mismatches 3; Indels 7; Conservative Query Match Best Local Similarity Matches 7; Conserv

1 MEKVQYLTRSAIRRA 15

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completed: October 1, 2004, 12:13:19 he : 63.2 secs Search con Job time :

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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RESULT 3
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APPLICANT: Coaska, Martti
APPLICANT: Coaska, Martti
APPLICANT: Videren, Jukka
APPLICANT: Videren, Jukka
APPLICANT: Videren, Jukka
APPLICANT: Videren, Timo
APPLICANT: Tilmen, Carola
APPLICANT: Tilmen, Carola
APPLICANT: Tilmen, Carola
APPLICANT: Compounds for Deactivating Phospholamban Function on TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 102.025001
CURRENT APPLICATION NUMBER: US/09/252,063
FALLE RAPLICATION NUMBER: US/09/252,063
FALLER APPLICATION NUMBER: 08/937,117
BARLIER PILING DATE: 1999-02-18
NUMBER: OF SEQ ID NOS: 10
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APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
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APPLICANT: Tilpertula-Ikonen, Marjo
APPLICANT: Tilpertula-Ikonen, Marjo
APPLICANT: Lotta, Timo
APPLICANT: Lotta, Timo
APPLICANT: Congounds for Deactivating Phospholamban Function on
ITLE OF INVENTION: Congounds for Deactivating Phospholamban Function on
ITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REPERENCE: 102.025001
CURRENT APPLICATION NUMBER: 08/99.22,063
CURRENT FILING DATE: 1999-02-18
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: cystolic part; OTHER INFORMATION: of phospholambam peptide US-09-252.063.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
100.0%; Score 75; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
ALIGNMENTS
                                                                                                                                      Sequence 9, Application US/09252063
Patent No. 6538022
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-05-252-063-1
; Sequence 1, Application US/09252063
; Patent No. 6538022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
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US-09-252-063-1
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LENGTH: 52
TYPE: PRT
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APPLICANT: Pollesello, Piero
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APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Marti
APPLICANT: Ovaska, Marti
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vilperttula-Ikonen, Marjo
APPLICANT: Tilgman, Carola
APPLICANT: Ariola Timo
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APPLICANT: Voaska, Marti
APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Piero
APPLICANT: Tenhunen, Jukka
APPLICANT: Tenhunen, Jukka
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Compounds for Deactivating Phospholamban Function on
ITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REPERBREC: 1102.025001
FILE REPERBREC: 1102.025001
CURRENT FILING DATE: 1999-02-18
FILE BAPLICATION NUMBER: 08/09/252,063
CURRENT FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn, Ver. 2.0
SOFTWARE: PatentIn, Ver. 2.0
SOFTWARE: PatentIn, Ver. 2.0
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Query Match
100.0%; Score 75; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Rattus sp.
US-09-252-063-5
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US-09-252-063-2
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APPLICANT: POllesello, Piero
APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Marti
APPLICANT: Tenhunen, Jukk
APPLICANT: Tigmann, Carola
APPLICANT: Tigmann, Carola
APPLICANT: Tigmann, Carola
APPLICANT: Tigmann, Carola
APPLICANT: Kaivola, Juha
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Ca-AFPESE (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
FILE REFERENCE: 192.02-063
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER FILING DATE: 1999-02-18
NUMBER OF SEO ID NOS: 10
SOFTMARE: PATENTIN VET. 2.0
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Query Match 100.0%; Score 75; DB 4; Length 52; Best Local Similarity 100.0%; Pred. No. 3e-07; Matches 16; Conservative 0; Mismatches 0; Indels
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GENDERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert 'Thierry
ITILE BOGGERT' THIETRY
ITILE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-04-15
PRIOR PILING DATE: 1999-06-01
NUMBER: OF SEQ ID NOS: 39
SOFTWARE: PATCHILIN VET: 2.0
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; Sequence 6, Application US/09252063
; Patent No. 6538022
                                                                                                1 MEKVOYLTRSAIRRAS 16
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Best Local Similarity 100.0
Matches 16; Conservative
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; ORGANISM: Homo sapiens
US-09-549-872B-15
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; ORGANISM: Mus sp.
US-09-252-063-6
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LENGTH: 52
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RESULT 8

US-09-252-063-3

Sequence 3, Application US/09252063

Patent No. 6538022

GENERAL INFORMATION:

APPLICANT: Ovaska, Martici

APPLICANT: Ovaska, Martici

APPLICANT: Ovaska, Martici

APPLICANT: Tidgren, Jukka

APPLICANT: Tidgren, Jukka

APPLICANT: Tidgren, Garlen

APPLICANT: Lotta, Timo

APPLICANT: Lotta, Timo

APPLICANT: Compounds for Deactivating Phospholamban Function on TITLE OF INVENTION: Campounds for Deactivating Phospholamban Function on TITLE OF INVENTION: Campounds for Deactivating Phospholamban Function on TITLE OF INVENTION: Campounds for Deactivating Phospholamban Inhibitors)

TITLE OF INVENTION: Campounds for Deactivating Phospholamban Function on TITLE OF INVENTION NUMBER: US/09/252,063

FULR REFERENCE: 1102.0255001

CURRENT APPLICATION NUMBER: US/09/252,063

EARLIER PILING DATE: 1999-02-18

SARIER PILING DATE: 1997-09-24

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: APPLICATION NUMBER: 200

LENGTH: APPLICATION NUMBER: 200

LENGTH: APPLICATION NUMBER: 200

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: APPLICATION NUMBER: 200

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Sequence 2, Application US/09252063;
Sequence 2, Application US/09252063;
Patent No. 6538022
GRNERAL INFORMATION:
APPLICANT: Oblesello, Piero
APPLICANT: Vidgren, Utkka
APPLICANT: Vidgren, Utkka
APPLICANT: Vidgren, Carola
APPLICANT: Vidgren, Carola
APPLICANT: Vidgren, Carola
APPLICANT: Cheta, Timo
APPLICANT: Cheta, Timo
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APPLICANT: Compounds for Deactivating Phospholamban Function on
APPLICANT: Applicant APPLICANT: Object
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Query Match 100.0%; Score 75; DB 4; Length 52
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 93.8'
Matches 15; Conservative
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; ORGANISM: Canis sp.
US-09-252-063-3
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US-09-252-063-2
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. Sequence 181, Application US/09732210 ; Patent No. 6573361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT.
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18000
                                                                                                  1 MEKVOYLTRSAIRRAS 16
                                                                                                                            1 MEKVQYITRSALRRAS 16
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Ouery Match
Best Local Similarity 87.5
Matches 14; Conservative
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APPLICANT: Pollesello, Piero
APPLICANT: Pollesello, Diero
APPLICANT: Pollesello, Dikka
APPLICANT: Videren, Jukka
APPLICANT: Videren, Jukka
APPLICANT: Videren, Jukka
APPLICANT: Vilgearuh, Carola
APPLICANT: Vilgearuh, Carola
APPLICANT: Lotta, Timo
APPLICANT: Lotta, Timo
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Ca-APPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.025001
FILE REFERENCE: 1999-02-18
FILE REFIGENT APPLICATION NUMBER: 08/937,117
BARLIER FILING DATE: 1999-02-18
FRALIER FILING DATE: 1999-02-18
FRALIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
                                                                           0
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                           ;
                         Query Match 96.0%; Score 72; DB 4; Length 52; Best Local Similarity 93.8%; Pred. No. 1.1e-06; Matches 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.0%; Score 72; DB 4; Length 52; Best Local Similarity 93.8%; Pred. No. 1.1e-06; Matches 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                    RESULT 9
US-09-549-872B-14

Sequence 14, Application US/09549872B

Patent No. 6540996

GENERAL INFORMATION:

APPLICANT: Zwaal, Richard

APPLICANT: Greenen, Jose

APPLICANT: Bogaert, Thierry

TITLE OF INVENTION: COMPOUND SCREENING METHODS

FILE OF INVENTION: COMPOUND SCREENING

CURRENT FILING DATE: 1000-04-14

PRIOR APPLICATION NUMBER: US/09/549,872B

CURRENT FILING DATE: 1999-04-15

PRIOR APPLICATION NUMBER: GB 9908670.4

PRIOR PILING DATE: 1999-04-15

PRIOR APPLICATION NUMBER: GB 9912736.7

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-04-15

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIN Ver. 2.0

SOFTWARE: PatentIN Ver. 2.0
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, Patent No. 6538022
                                                                                                                                                      1 MDKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDKVQYLTRSAIRRAS 16
                                                                                                                            1 MEKVOYLTRSAIRRAS 16
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ORGANISM: Gallus sp.
US-09-252-063-7
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US-09-252-063-7
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                                                                           Matches
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| Query Watch | 94.7%; Pred, Proc. 71; Pred; Proc. 71; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Proc. 72; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; Pred; P
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US-09-252-991A-24791

Sequence 24791, Application US/09252991A

Sequence 24791, Application US/09252991A

Sequence 24791, Application US/09252991A

Setent No. 6551795

TERENTAL INFORMATION: MUCLEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: MUCLEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: MUGHER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PAPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24791
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                                                                                                                                                                                                                                                                                   Length 686;
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Sequence 18, Application US/08588983
Sequence 18, Application US/08588983
Fatent No. 5854667
GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: for Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: IX
COUWIRY: US
ZIP: 77210
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                                                                                                                                                                                                                                                                        Query Match

48.0%; Score 36; DB 4; I
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            TYPE: PRT / ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 50.00
For 17 Conservative
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                         NUMBER OF SEQ ID NOS:
SEQ ID NO 19332
LENGTH: 686
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PRIOR FILING DATE:
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITL
                                    IS-09-489-039A-7319
Sequence 7319, Application US/09489039A
Patent No. 661083B
Patent No. 661083B
Patent No. 661083B
Patent No. 661083B
Patent No. 661083B
Patent No. 661083B
Patent No. 661083B
Patent No. 661083B
Patent No. 661081B
Patent Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2009-004001
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NO 7319
FERMAND NO. 7319
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FAPPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11071
LENGTH: 194
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Pred. No. 15;
3; Mismatches 2; Indels
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Patent No. 6610836
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US-09-489-039A-7319
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CRGANISM: Klebsiella pneumoniae
US-09-489-039A-11071
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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51 KPQHLTRSGMRK 62
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US-09-252-991A-19332
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RESULT 19
US-09-252-991A-28362
; Sequence 28362, Application US/09252991A
; Sequence 28362, Application US/09252991A
; Patent No. 651795
; GENERAL INFORMATION:
; TITLE OF INVENTION: Marc J. Rubenfield et al.
; TITLE OF INVENTION: MARC J. MOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: MOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: MORBER: US/09/252,991A
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR PELING DATE: 1998-02-18
; PRIOR PELING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28362
; LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCOMMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
FILE REFERENCE: GTC-007
CURRENT PILLING LOATE: 1998-08-13
PRIOR PILLING DATE: 1997-11-08
PRIOR PILLING DATE: 1997-11-08
PRIOR FILLING DATE: 1997-11-08
PRIOR FILLING DATE: 1997-108-14
NUMBER: OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
SEQ ID NOS: 5674
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; Ratent No. 6671156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; FILE REFERENCE: 032796-032
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46.7%; Pred. No. 54;
tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5136, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT , ORGANISM: Staphylococcus epidermidis US-09-134-001C-5136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 EKVDFLTKEIERRTT 196
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Best Local Similarity 46.74
Matches 7; Conservative
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US-09-134-000C-6395
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48.0%; Score 36; DB 2; Length 924;
Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels
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Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/08588976
Patent No. 5891717
GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Inhibiting Hexokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,976
FILING DATE: Concurrently herewith
CLASSIFICATION: APPLICATION: APPLICATION: APPLICATION ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUTICATION INFORMATION:
TELECHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: FUSSEY, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:481/FUS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amin
                                                                                                                                                                          TELEX: n/a
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  LENGTH: 924 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-588-976-18
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ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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US-08-588-976-18
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638 ODVVYLLREAIRR 650

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Score 35; DB 4; Length 357;
Pred. No. 97;
2; Mismatches 0; Indels
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; Sequence 4, Application US/09277262
; Patent No. 6395482
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                               Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative 2
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Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                  313 KKIQYLTR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mus musculus
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-277-262-2
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Batent No. 6635750

GENERAL INFORMATION

APPLICANT: Coyle, Anthony J.

APPLICANT: Fraser, Christopher C.

APPLICANT: Manning, Stephen

TITLE OF INVENTION: Pamily and Uses Thereof

TITLE OF INVENTION: Pamily and Uses Thereof

TITLE OF INVENTION: Pamily and Uses Thereof

CURRENT APPLICATION NUMBER: US/09/620,461

CURRENT APPLICATION NUMBER: US/09/620,461

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 14

LENGTH: 357
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US-09-910-174B-14

Sequence 14, Application US/09910174B

Patent No. 6630575

JERNERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Braser, Christopher C.
APPLICANT: Braser, Christopher C.
TITLE OF INVENTION: Family and Uses Thereof
TITLE OF INVENTION: Family and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/910,174B

CURRENT FILING DATE: 2001-07-20

PRIOR FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 32

SOFTWARER: FastSEQ for Windows Version 4.0

LENGTH: 357
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Pred. No. 56;
2; Mismatches 4
CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SEQ ID NO 6395 LENGTHARE: Patentin version 3.1 LENGTH: 216
                                                                                                                                                         TYPE: PRT ; ORGANISM: Enterococcus faecalis US-09-134-000C-6395
                                                                                                                                                                                                                                               46.7%;
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Best Local Similarity 50.0
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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ORGANISM: Homo sapiens
US-09-910-174B-14
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ORGANISM: Homo sapiens
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US-09-620-461-14
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GENERAL INFORMATION:

APPLICANT: Karaylorgou, Maria
APPLICANT: Karaylorgou, Maria
APPLICANT: Karaylorgou, Maria
APPLICANT: Gogos, Joseph A
TITLE OF INVENTION: METHODS OF DETERMINING A SUSCEPTIBILITY TO OR PRESENCE
TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
FILE PERRENCE: 600-1-223 CIP
FILE REPERENCE: 600-1-223 CIP
CURRENT APPLICATION NUMBER: US/09/277,262
EARLIER APPLICATION NUMBER: US/09/277,262
EARLIER FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2 Application US/09277262

Sequence 2 Application US/09277262

Patent No. 6395482

GENERAL INFORMATION:
APPLICANT: Karayiozegu, Maria
APPLICANT: Karayiozegu, Maria
APPLICANT: Gogos, Joseph A

TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
TITLE OF INVENTION NUMBER: US/09/277,262
CURRENT PELLOR DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/229,530
EARLIER PLING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VEY: 2.0
SOFTWARE: PATENTIN VEY: 2.0
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43.8%; Pred. No. 1.5e+02;
tive 4; Mismatches 5; Indels
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Search completed: October 1, 2004, 12:21:12 Job time: 18 secs

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Total number

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Title: Perfect

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Result No.

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Sequence 16, Appl
Sequence 18, Appl
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Sequence 4722, A
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Sequence 39, Appl
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Sequence 1
Sequence 5
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US-09-954-571-4
US-09-954-571-2
US-10-705-791-15
US-10-705-791-17
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1 MEKVQYLTRSAIRRAS 16
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US-10-705-791-10

US-10-705-791-10

Sequence 10, Application US/10705791

Sequence 10, Application US/10705791

Sequence 10, Application No. US2040121942A1

GENERAL INFORMATION:

APPLICANT: The Regents of the University of California

APPLICANT: Chief, Kenneth

APPLICANT: Minamisawa, Susanne

APPLICANT: He, Huapling

APPLICANT: He, Huapling

APPLICANT: He, Huapling

APPLICANT: Scott, Christopher

APPLICANT: Scott, Christopher

APPLICANT: Warkus

APPLICANT: Warkus

APPLICANT: Warkus

APPLICANT: Warkus

APPLICANT: Warkus

APPLICANT: Soft, Christopher

APPLICANT: Silverman, Gregg J.

TITLE OF INVENTION: OF CARPIAC DISEASE

FILE REFERBNCE: 6627-PA9025

CURRENT APPLICATION NUMBER: US/10/705,791

CURRENT PLING DATE: 1999-11-02

FRIOR FILING DATE: 1999-11-02

NUMBER OF SEG ID NOS: 19

SEQ ID NO 10

LENGTH: 36

LENGTH: 36

LENGTH: 36

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LENGTH: 36
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
REGORD FOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 11
LENGTH: 35
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Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0;
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Sequence 2, Application US/09954571

Publication No. US20202032167A1

CENERAL INFORMATION:

APPLICANT: Chien, Kenneth R
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CRGANISM: Homo sapiens
US-10-705-791-10
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-10-705-791-11
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Best Local Similarity
Matches 16; Conservat
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GENERAL INFORMATION:

APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Chien, Kenneth
APPLICANT: Chien, Kenneth
APPLICANT: Minamisawa, Susanne
APPLICANT: Ho, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Soct, Chistopher
APPLICANT: Soct, Chistopher
APPLICANT: Soct, Chistopher
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Whuser: Us/10/705,791
CURRENT APPLICATION NUMBER: Us/10/6,718
FILE REPRENCE: 6627-PA9025
FILE REPRENCE: 6627-PA9025
FILE REPRENCE: 6627-PA9025
FILE REPRENCE: 6627-PA9025
FILE REPRENCE: 6627-PA9025
FILE REPRENCE: 6627-PA9025
FILE REPRENCE: 6627-PA9025
FILE REPRENCE: 6627-PA9025
FILE REPRENCE: 667-PA9025
FILE REPRENCE: 66
                                                                                                                                  442, App
442, App
464, App
71171, A
57201, A
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Sequence 2255, Ap
Sequence 52269, A
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Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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Sequence 11, Application US/10705791
Sequence 11, Application US/20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Chien, Kenneth
APPLICANT: Minamisan, Wolfgang
APPLICANT: Minamisan, Susanne
                                                                           US-10-282-122A-61911
US-10-437-963-103091
US-10-372-964-42
US-10-097-065-442
US-10-112-944-464
US-10-282-122A-71171
US-10-282-122A-71171
US-10-093-463-164
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US-10-425-114-52269
                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/10705791 Publication No. US20040121942A1 GENERAL INFORMATION:
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Hoshijima, Masahiko
Meyer, Markus
Scott, Christopher
Wang, Yibin
Silverman, Gregg J.
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ORGANISM: Homo sapiens
                                     US-10-705-791-8
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APPLICANT:
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Gaps

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APPLICANT: Zhang, Bing
APPLICANT: Glabson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glabson, Bradford W.
APPLICANT: Glann, Gary M.
APPLICANT: Glann, Gary M.
APPLICANT: Warnock, Dale E.
ITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                           Score 75; DB 12; Length 52;
Pred. No. 1.9e-06;
Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-371-101-15
Sequence 15, Application US/10371101
Publication No. USC030149995A1
Sequence 15, Application US/10371101
Sublication No. USC030149995A1
Sequence 15, Application US/10371101
Substance 1 Proceeding 1 Proceeding 1 Proceeding 1 Proceeding 1 Proceeding 1 Proceeding 1 Proceeding 1 Proceeding 1 Proceeding 2 Proceeding 2 Proceeding 1 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 2 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 3 Proceeding 
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Sequence 478, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: FAPY, Edin D.
                  ; NUMBER OF SEQ ID NOS: 5
; SOFWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-954-571-5
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Best Local Similarity 100.0
Matches 16; Conservative
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TYPE: PRT
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## APPLICANT: Hoshijima, Masahiko
## APPLICANT: Ross, John
## APPLICANT: Ross, John
## APPLICANT: Ikeda, Yasuhiro
## TITLE OF INVENTION: HIGH BFFICIENCY CARDIAC GENE TRANSFER
## TITLE OF INVENTION: HIGH BFFICIENCY CARDIAC GENE TRANSFER
## CURRENT APPLICATION NUMBER: US/09/954,571
## CURRENT FILING DATE: 2001-09-11
## PRIOR FILING DATE: 2000-11-09
## NUMBER OF SEQ ID NOS: 5
## SOFTWARE: Patentin Version 3.2
## SEQ ID NO 2
## ILENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 75; DB 12; Length 52; 100.0%; Pred. No. 1.9e-06; Ive 0; Mismatches 0; Indels
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Publication No. US2020032167A1
GENERAL INPORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ross, John
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT APPLICATION DATE: 2001-0911
PRIOR FILING DATE: 2000-11-09
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Ouery Match

Best Local Similarity 100.0%; Pred. No. 1.9e-06;

Matches 16; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-571-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
US-09-954-571-4
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Gaps

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APPLICANT: He, Huaping, Assahiko
APPLICANT: Hoshijian, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Silverman, Greeg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: MERER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR APPLICATION NUMBER: PT/US99/25692
PRIOR APPLICATION NUMBER: PT/US99/25692
PRIOR APPLICATION NUMBER: PT/US99/25692
PRIOR PILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin'version 3.2
SEQ ID NO 17
LENGTH: 79
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Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Dillmann, Wolfgang APPLICANT: Diamamisawa, Susanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0;
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-111-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 52
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; ORGANISM: Escherichia coli
US-10-705-791-17
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CRGANISM: Homo sapiens
US-10-705-791-2
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US-10-705-791-19
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GENERAL INFURMATION:
APPLICANT The Regents of the University of California
APPLICANT Chien, Kenneth
APPLICANT Chien, Kenneth
APPLICANT Dillmann, Wolfgang
APPLICANT He, Huaping
APPLICANT He, Huaping
APPLICANT Goot, Christopher
APPLICANT: Hoshijina, Masahiko
APPLICANT: Mang, Yibin
APPLICANT: Mang, Yibin
APPLICANT: Scott, Christopher
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TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
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Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 75; DB 16;
100.0%; Pred. No. 1.9e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                100.0%; Score 75; DB 16;
100.0%; Pred. No. 1.9e-06;
:ive 0; Mismatches 0;
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Publication No. US20040121942A1
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Hoshijima, Masahiko
Meyer, Markus
Scott, Christopher
Wang, Yibin
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Dillmann, Wolfgang
Minamisawa, Susanne
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Best Local Similarity 100.0
Matches 16; Conservative
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ORGANISM: Homo sapiens
                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 16; Conserva
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                                                                                                                                            US-10-408-765A-478
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APPLICANT:
APPLICANT:
                         ; SEQ ID NO 478
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APPLICANT:
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APPLICANT: Minamiswa, Susanne
APPLICANT: Minamiswa, Susanne
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: Grot Markus
APPLICANT: Scott, Christopher
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APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: METHOR FOR INVENTION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT APPLICATION NUMBER: G0/106,718
PRIOR APPLICATION NUMBER: G0/106,718
PRIOR APPLICATION NUMBER: PT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PALENTH VERSION 3.2
LENGTH: 52
LENGTH: 52
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                                                                                                                 TITLE OF INVENTION: COMPOUND SCREENING METHODS FILE REFERENCE: D00590.7005.US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
FRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: US 60/129,596
FRIOR APPLICATION NUMBER: US 60/129,596
FRIOR FILING DATE: 1999-04-15
FRIOR FILING DATE: 1999-06-01
FRIOR FILING DATE: 1999-06-01
FRIOR FILING DATE: 2090-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATCHTING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATCHTING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATCHTING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATCHTING DATE: 2000-04-14
SEQ ID NO 14
LENGTH: 52
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93.8%; Pred. No. 6.9e-06;
tive 1; Mismatches 0,
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US-10-705-791-13
; Sequence 13, Application US/10705791
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Publication No. US20040121942A1
GENERAL INFORMATION:
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Best Local Similarity 93.8³
Matches 15; Conservative
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Best Local Similarity 93.83
Matches 15; Conservative
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APPLICANT: He, Haaping
APPLICANT: Hoshijima, Masahko
APPLICANT: Hoshijima, Masahko
APPLICANT: Moser, Markus
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: OF CARRIAC DISEASE
FILE REPRENCE: 6627-PA9025
FILE REPRENCE: 6627-PA9025
CURRENT PAPLICATION NUMBER: US/10/705,791
CURRENT PAPLICATION NUMBER: 60/106,718
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
TYPE. ...
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Publication No. US20030149995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
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US-10-705-791-19
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US-09-954-571-3
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Best Local Similarity 93.8
Matches 15, Conservative
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US-10-371-101-14
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APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Markus
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT;
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT;
TITLE OF INVENTION: MUMBER: W110/705,791
CURRENT APPLICATION NUMBER: 60/106,718
FRICK APPLICATION NUMBER: 60/106,718
FRICK APPLICATION NUMBER: FOT/US99/25692
FRICK APPLICATION NUMBER: PCT/US99/25692
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Sequence 1, Application US/09954571

Publication No. US20020032167A1

GENERAL INFORMATION:

APPLICANT: Chien, Kenneth R

APPLICANT: Ross, John

APPLICANT: Ikeda, Yasuhiro

TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER

FILE REFERENCE: 6627-PA0123

CURRENT FILING DATE: 2001-09-11

PRIOR PILING DATE: 2000-11-09

NUMBER: OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.2

SEQ ID NO 1

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Pred. No. 1.1e-05;
0; Mismatches 0;
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Best Local Similarity 100.0%; P
Matches 15; Conservative 0;
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Dillmann, Wolfgang
Minamisawa, Susanne
He, Huaping
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GRGANISM: Escherichia coli
US-10-705-791-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial
FEATURE:
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APPLICANT: Scott Christopher
APPLICANT: Scott Christopher
APPLICANT: Scott Christopher
APPLICANT: Sloverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
TILE REFERENCE: 6627-PA0025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT PRING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR PLING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
LENGTH: 35
LENGTH: 35
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94.7%; Score 71; DB 16; Length 36

Best Local Similarity 100.0%; Pred. No. 7.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                           APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Dillmann, Wolfgang APPLICANT: Minamisawa, Susanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.7%; Score 71; DB 16; I
100.0%; Pred. No. 6.9e-06;
iive 0; Mismatches 0;
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APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF
TITLE OF INVENTION: METHOD FOR INHIBITION OF
TITLE OF INVENTION: METHOD FOR INHIBITION OF
TITLE OF INVENTION: MOMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTION TO NUMBER: PCT/US99/25692
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 12
LENGTH: 36
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Dillmann, Wolfgang
Minamisawa, Susanne
                                                                                                                                                                                                                                                  He, Huaping
Hoshijima, Masahiko
Meyer, Markus
tion No. US20040121942A1
INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
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US-10-705-791-12
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, ORGANISM: Homo sapiens
US-10-705-791-13
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APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: He, Huaping
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Sliverman, Gregor
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Warthook FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
TITLE OF INVENTION: OF CARDIAC DISEASE
CURRENT PLING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Anou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICANT: NUMBER: US/10/424,599
KURBEN OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                             Query Match
92.0%; Score 69; DB 16;
Best Local Similarity 93.8%; Pred. No. 2.5e-05;
Matches 15; Conservative 0; Mismatches 1
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Publication No. US20040121942A1
GENERAL INFORMATION:
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            NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                    1 MEKVQYLTRSAIRRAS 16
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                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-705-791-3
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US-10-705-791-6
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Best Local Similarity
Matches 14; Conserv
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                                                           SEQ ID NO 3
LENGTH: 52
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APPLICANT: Chien, Kenneth
APPLICANT: Chien, Kenneth
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minanisawa, Susanne
APPLICANT: Minanisawa, Susanne
APPLICANT: Minanisawa, Susanne
APPLICANT: Sout, Chistopher
APPLICANT: Sout, Chistopher
APPLICANT: Mayor, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
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APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: PRINT WANGER: US,10,705,791
CURRENT FILING DATE: 1998-11-02
PRIOR PILING DATE: 1998-11-02
PRIOR PILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
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CURRENT APPLICATION NUMBER: 60/106,718
PRIOR APPLICATION NUMBER: CT/US99/25692
PRIOR PILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
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Pred. No. 1.7e-05;
); Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Dillmann, Wolfgang
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                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10705791
Publication No. US20040121942A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
Best Local Similarity 100.0%; P. Matches 15; Conservative 0;
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Dillmann, Wolfgang
Minamisawa, Susanne
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                                                                                    1 MEKVOYLTRSAIRRA 15
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; ORGANISM: Homo sapiens
US-10-705-791-4
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APPLICANT:
APPLICANT:
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; LENGTH: 116
; TYPB: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10177
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1 General 44-46161

2 Sequence 46161, Application US/10425114

3 Publication No. US20040034888A1

GENERAL INPOWNATION:

3 APPLICANT: Dist, Jingdong

3 APPLICANT: Dist, Yilua

4 APPLICANT: Tabaska, Jack E

4 APPLICANT: Tabaska, Jack E

5 APPLICANT: Tabaska, Jack E

5 APPLICANT: Cao, Yongwei

7 ITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

7 ITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

7 ITLE OF INVENTION: Nucleic Acid Molecules Associated With

7 ITLE OF INVENTION: Nucleic Acid Molecules Associated With

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Best Local Similarity 71.4%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 12; Length 44; Pred, No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                          , OTHER INFORMATION: Clone ID: PAT_MRT3847_57573C.1.pep
US-10-424-599-238702
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Sequence 10177, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION

APPLICANT: CMURA, SATOSHI

APPLICANT: ISHIKAWA, UNN

APPLICANT: SHIKAWA, UNN

APPLICANT: SHIKAWA, UNN

APPLICANT: SHIRAW, HROSHI

APPLICANT: SHIRAY, TADAYOSHI

APPLICANT: SHIRAY, TADAYOSHI

APPLICANT: SHIRAY, 10SHIVKI

APPLICANT: HATTON! NOVEL POLYNUCLEOTIDES

FILE REPERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-39

PRIOR PLLING DATE: 2001-05-30

PRIOR PLING DATE: 2001-05-30
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25 LEKIEYITRERIK 37
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                                                                                                                   TYPE: PRT ORGANISM: Glycine max
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Score 41; DB 14; Length 116;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule; type: mRNA
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A; Molecule; type: mRNA
A; Cross-references: GB: S95849; NID: 9247934
C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm Pase; after phosphorylation, the calcium pump is activated and the rate of muscle relaxat C; Superfamily: phospholamban
C; Keywords: acetylated amino end; ATPase inhibitor; cardiac muscle; heart; pentamer; phos
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F;1/Modified site: acetylated amino end (Met) #status predicted
F;1/Modified site: acetylated amino end (Met) #status predicte
F;1/Modified site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predicte
F;1//Ainding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status pr
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Richanahan, C.W.; Weissberg, P.L.; Metcalfe, J.C.
Circ. Res. 73, 193-204, 1953
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A; Readues: 1522 caudha and A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A; Residues: 1-52 caudha A;
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F:1/Modified site: acetylated amino end (Met) #status predicted
F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Cross-references: GB:M63603; NID:g189942; PIDN:AAA60083.1; PID:g189943
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is C;Comment: Helical transmembrane domains of five chains are thought to aggregate in the
                                                                                                                                                                                                                                                                                                                                                                                                                                              cloning of the human cDNA, and assi
                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Azere Se-Reb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Accession: A40424
R;Fujii, J; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
B;Pujii, J.; Zarain-Firsperg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
A; Biol. Chem. 266, 11669-11675, 1991
A;Title: Structure of the rabbit phospholamban gene, cloning of the human cDA;Reference number: A40424; MUID:91268032; PMID:1828805
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A;Residues: 1-52 <HWA1>
A;Cross-references: GB:S95853; NID:g247932; PIDN:AAB21903.1; PID:g247933
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ALIGNMENTS
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A,Cross-references GDB:128300; OMIM:172405
A,Map Dossition: 6922.1-6922.1
C,Superfamily: phospholamban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEKVQYLTRSAIRRAS 16
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Best Local Similarity 100.03
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-52 <FUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A40424
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                                                                                                                                                                                                     phospholamban
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phospholamban - rabbit (domestic rabbit)

() Species: Oryctolagus cuniculus (domestic rabbit)

() Species: Oryctolagus cuniculus (domestic rabbit)

() Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999

() Accession: B40424; S00249

R;Fujii, J: Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.

R;Fujii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, Chem. 266, 11669-11669, 1991

A;Fujii. J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.

A;Fujii. J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.

A;Feference number: A40424, MUD: 91268032; PMID: 1828805

A;Accession: B40424

A;Accession: B40424

A;Residues: 1-52 <FUG.

A;Cross-references: GB: M63601; NID: 9165636; PIDN: AAA31445.1; PID: 9165639
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Gaps
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A;Accession: 146227
A;Accession: translated from GB/EMBL/DDBJ
A;Accession: translated from GB/EMBL/DDBJ
A;Accession: translated from GB/EMBL/DDBJ
A;Accessive translated mana
A;Accessive translated mana
A;Cross-references: GB:M3539; NID:g164045; PIDN:AAC41618.1; PID:g164046
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
C;Comment: Phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation in
C;Reywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tri
C;Reywords: acetylated amino end (Met) #status experimental
F;31-52/Domain: transmembrane #status predicted <TWM>
F;11/Modified site: acetylated amino end (Met) #status experimental
F;16/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status experim
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: phospholamban
C; Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tra
C; Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; transmembrane #status predicted aTMN>
F; 17 Modified site: acetylated amino end (Met) #status predicted
F; 16 Asinding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicte
F; 17 Asinding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status pr
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C.Species: Sus scrofta domestica (domestic pig)
C.Species: Sus scrofta domestica (domestic pig)
C.Date: 21-Nov-1993 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C.Accession: 805540
R.Yerboomen, H.; Muytack, F.; Eggermont, J.A.; de Jaegere, S.; Missiaen, L.; Raeymaekers
Bochem. J. 262, 353-356, 1989
A.Title: cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle.
A.Reference number: 805540; MUID:90056437; PMID:2530978
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C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a chicken phospholamban.
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C;Species: Gallus gallus (chicken)
C;Species: 06-Mar-1992 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Accession: A39535; B39535; A44531
R;Toyofuku, T.; Zak, R.
J;Biol. Chem. 266, 5375-5383, 1991
A;Fille: Characterization of cDNA and genomic sequences encoding a chicken IA;Reference number: A39535; MUID:91170195; PMID:1825996
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A; Molecule type: mRNA
A; Residues: 1-17, 'I', '19-52 <TOY>
A; Residues: 1-17, 'I', '19-52 <TOY>
A; Residues: GB: M59039; NID: g212575; PIDN: AAA62738.1; PID: g212576
A; Note: the authors translated the codon CTT for residue 18 as Ile
A; Accession: B39535
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Pred. No. 2e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 52;
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93.8%; Pred. No. 2e-06;
live 1; Mismatches
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Best Local Similarity 93.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
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Best Local Similarity
Matches 15; Conserv
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A; Residues: 1-52 <VER>
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                                                                                                               the same phospholamban gene
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R;Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H.
FEBS Lett. 227, 51-55, 1988
A;Title: Robit cardiac and slow-twitch muscle express t
A;Reference number: S00249; MUID:88112222; PMID:2262883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 75; DB 1; I
100.0%; Pred. No. 5.4e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                          A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-52 <FU2>
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Best Local Similarity 100.
Matches 16, Conservative
                                                                                                                                                                                                 A; Accession: S00249
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C, Genetics:
A, Gene: PH0606
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A; Residues: 1-52 <702.
A; Cross_references: GB:M59038
A; Note: the sequence of residues 33-52 and the corresponding nucleotide sequence are not A; Note: the sequence of residues 33-52 and the corresponding nucleotide sequence are not R; Toyofuku, T.; Zak, R.
submitted to GenBank, April 1991
A; Reference number: A44531
A; Molecule type: DNA
A; Residues: 1-52 <703-
A; Cross-references: GB:M39038
A; Cross-references: GB:M39038
A; Cross-references: GB:M39038
C; Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and C; Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplast C; Comment: Phospholamban is the major phosphorylated and the rate of muscle relaxation is c; Genetics:
A; Note: only one gene was detected
A; Note: only one gene was detected
A; Note: only phospholamban
C; Genetics:
A; Note: only phospholamban
C; Keywords: accrylated amino end; ATPase inhibitor; muscle; pentamer; phosphorotein; tr
C; Keywords: accrylated amino end (Met) #status predicted
F; 11/Modified site: accrylated amino end (Met) #status predicted
F; 11/Binding site: phosphate (Gar) (covalent) (by caMP-dependent kinase) #status F; 11/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent Kinase)
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C.Species: Pyrococcus abyssi
C.Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C.Accession: F75089
R. anonymous, Genoscope
S. anonymous, Genoscope
R. anonymous, Genoscope
R. A. Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A. Reference number: A75001
A. Accession: F75083
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Cispecies: Streptomyces coelicolor

Cispecies: Streptomyces coelicolor

Cispecies: Streptomyces coelicolor

Cidacession: T34780

R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

A;Reference number: Z21557

A;Recession: T34780

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

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A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDB
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Species: Streptomyces coelicolor
Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.7%; Score 71; DB 1; Length 52; 87.5%; Pred. No. 3e-06; 1:ve 2; Mismatches 0; Indels
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Best Local Similarity 46.7
Matches 7; Conservative
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Matches 1
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ribosomial protein L19 (rplS) - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Accession: B70187
C;Accession: B70187
C;Accession: B70187
C;Accession: B70187
C;Accession: B70187
C;Accession: B70187
C;Accession: B70187
C;Accession: B70187
C;Accession: B70187
C; Cotton, M.D.; Horst, R.; Lathigra, R.; White, son, D.; Acrland, S.; Fujil, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hanson, M.; Vugt, Arthers 390, 580-586, 1997
C; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
C; Cotton, M.D.; Horst, Y.; Roberts, K.; Hatch, B.
C; Cotton, M.D.; Horst, J.C.
C; Cotton, M.D.; Horst, K.; Roberts, R.; Hatch, B.
C; Status: preliminary; nucleic acid sequence not shown; translation not shown
C; A; Cotton: A; Cotton, M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M.D.; M
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C;Accession: E71104
R;Käwarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamoto, S; Sekine
M; Ohfuku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguchi,
DNA Res: 5, 55-76, 1998
A;Pitle: Complete sequence and gene organization of the genome of a hyper-thermophilic as
A;Reference number: A;1000; MUID:98344137; PMID:9679194
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A;Residues: 1-1108 <KAW>
A;Cross-references: GB:Ap000003; NID:g3236130; PIDN:BAA29695.1; PID:d1030638; PID:g325701
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                     GB:AL096836; NID:g5458366; PIDN:CAB49971.1; PID:g5458487
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                    54.7%; Score 41; 50.0%; Pred. No.
A; Molecule type: DNA
A; Residues: 1-451 < RAN>
A; Cross-references: GB:A4248286; GB:A1
A; Experimental source: strain Orsay
C; Genetics:
A; Gene: PAB1666
C; Superfamily: phosphomannomutase
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435 MEKAEKLVKDAIKKAS 450
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Best Local Similarity 53.3%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.07
Local 8; Conservative
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nes 8; Conservative
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A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Accession: H69179
A; Atatus: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-283 AMIT>
A; Cross-references: GB:AE000842; GB:AE000666; NID:g2621676; PIDN:AAB85107.1; PID:g262168
A; Genetics:
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Abote: Nostoc sp. Btrain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Accession: AC1867
C;Accession: AC1867
Nakazari, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yamada, M.; Tabata, S. Natile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15547.1; PID:e117388
A;Experimental source: strain H37Rv
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C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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(7)
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Pred. No.
                           Bacteriol. 179, 7135-7155, 1997
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Best Local Similarity 63.6
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209 YLTREAFKRAA 219
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D69155
hypothetical protein MTH425 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Decies: Methanobacterium thermoautotrophicum
C;Decies: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ciu, D.; Speafcra, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Recience number: A69000; MUID:98037514; PMID:9371463
A;Residues: 1-119 cMTH>
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Cipate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

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Rianonymous, Genoscope
submitted to the EMBL Data Library, July 1999

Alpostiption: Pyrococcus abysesi genome sequence: insights into archaeal chromosome structure and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and alphaners and a
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H69179
conserved hypothetical protein MTH601 - Methanobacterium thermoautotrophicum (strain Del
c)Species: Methanobacterium thermoautotrophicum
c)Species: Methanobacterium thermoautotrophicum
C)Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000
C)Accession: H69179
R.Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
R.Smith, D.R.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
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                                                                                                                                                                                                                                                                                                                    hypothetical protein PAB0334 - Pyrococcus abyssi (strain Orsay)
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30;
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Pred. No.
|| || || || :| :| || MEVKDYLTREEVRKA 682
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Best Local Similarity 50.0%;
Matches 7; Conservative
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C, Genetics:
A, Gene: PA1212
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77.8%;
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58.3%;
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
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F83493
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N;Alternate names: dTDP-4-keto-L-rhamnose reductase
C;Species: Actinobacillus actinomycetemcomitans
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C;Species: Arabidopsis thaliana (Mouse-ear cress)
C;Date: 23.Apr.1999 #sequence_revision 23.Apr.1999 #text_change 23.Jul.1999
C;Date: 23.Apr.19913
R;Respend: M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, November 1998
A;Refearce number: Z15398
A;Residues: 1-2712 *ABD.
A;Residues: 1-2712 *ABD.
A;Residues: 1-2712 *ABD.
A;Residues: 1-2712 *ABD.
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Best Local Similarity 63.6%; Pred. No. 4.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels
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Length 308;
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    DB 2;
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4; Mismatches
    Score 37; DB Pred. No. 44; 3; Mismatches
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Best Local Similarity 46.7%; Pred. No. 5
Matches 7; Conservative 4; Mismatch
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210 VEKLEYLNERAIPRS 224
    49.3%;
ilarity 53.3%;
Conservative
                                                                                                                                                                                                                                         1 MEKVOYLTRSAIRRA 15
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1473 LEKVEWLARSA 1483
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                                                   Best Local Similarity
Matches 8; Conserv
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                  Query Match
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C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession: T00104
R;Nakano, Y; Yoshida, Y:, Yamashita, Y:, Koga, T.
B;Nakano, Y; Yoshida, Acta 1444, 1998
B;Nakano, Y; Yoshida, Acta 1444, 1998
B;Nakano, Y; Yoshida, Acta 1444, 1998
B;Nakano, Y; Yoshida, Acta 1444, 1998
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B;Nakano, Y; Yoshida, Acta 1444, 1998
B;Nakano, Yoshida, Acta 1444, 1998
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B;Nakano, Yoshida, Accession: T00104
B;Nakano, Yoshida, Accession: Maliabolo415; NID:G3132248; PIDN:BAA28133.1; PID:G3132256
B;Nakano, Yoshida, Accession: Strain NCTC 9710
C;Function:
A;Packanida: Surves strain NCTC 9710
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Frol) (c;Species Pseudomonas aeruginosa ceruginosa pada, x.o. bran, y., brody, s., olson, M.V. a., coller, s., coller, s., coller, s., coller, s., coller, coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., coller, s., 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Pred. No. 74;
3; Mismatches 2; Indels
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Best Local Similarity 61.5%; Pred. No. 4
Matches 8; Conservative 1; Mismatch
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N,Alternate names: protein F20B18.190
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;bate: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C;Accession: T04263; A54588
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: AH1053
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Atthors: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Accession: AH1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis tha A;Reference number: A54588; MUID:94255767; PMID:8197457
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A;Cross-references: GB:AL513382; PIDN:CAD06877.1; PID:g16505525; GSPDB:GN00176
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-104,'V',106-434 <MEY>
A;Cross-references: GB:X78886; NID:g509418; PIDN:CAA55484.1; PID:g509419
                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphoprotein phosphatase (EC 3.1.3.16) ABII - Arabidopsis thaliana
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                                                                                                                       DB 2;
93;
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                                                                                                                       Score 36;
Pred. No.
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C, Keywords: phosphoric monoester hydrolase
     A, Experimental source: strain PAO1
C, Genetics:
A, Gene: hcnC, PA2195
                                                                                                                    48.0%;
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A;Residues: 1-434 <BEV>
A;Cross-references: EMBL:AL049483
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Best Local Similarity 50.v.
7; Conservative
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A, Introns: 183/3; 280/3; 316/1
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Cippete: 13-Aug-1999
Reaguance_revision 13-Aug-1999 #text_change 15-Oct-1999
Cipcetes: Bacillus subtilis phage SPEC2
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Best Local Similarity 58.3
Matches 7; Conservative
     Conservative
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A;Gene: STY4756

Query Match
Best Local Similarity 53.8%; Pred, No. 1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels.

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2 EKVQYLTRSAIRR 14 :|| ::|| || 294 DKVTWMTREASRR 306

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Search completed: October 1, 2004, 12:19:44 Job time : 16.6 secs

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H44 ARATH

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RIAURE R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruelan K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Maruelan K., Carmin G.M., Hong L., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glabs R.A., Rhiting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Schieln J.E., Jones S.J.M., Marra M.A., Schieln J.E., Jones S.J.M., Marra M.A., Rohnich Length
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MEDLINE-91268032; PubMed=1828805;
Fujil J., Zarain-Herzberg A., Willard H.F., Tada M., Maclennan D.H.;
"Structure of the rabbit phospholamban gene, cloning of the human
CDNA, and assignment of the gene to human chromosome 6.";
J. Biol. Chem. 266:11669-11675(1991).
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MEDLINE=95269058; PubMed=7749920;
Adams P.D., Arkin I.T., Engelman D.M., Bruenger A.T.;
"Computational searching and mutagenesis suggest a structure for the pentameric transmembrane domain of phospholamban.";
Nat. Struct. Biol. 2:154-162(1995).
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McTiernan C.F., Frye C.S., Lemster B.H., Kinder B.A., Ogletree-Hughes M.L., Moravec C.S., Feldman A.M.; "The human phospholamban gene: structure and expression."; J. Mol. Cell. Cardiol. 31:679-692(1999).
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Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB).
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MEDLINE=99222499; PubMed=10198197;
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MEDLINE=95298769; Pubmed=7779806;
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MEDLINE=98170970; PubMed=9512019;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rattus norvegicus. (Rat), and Oryctolagus cuniculus (Rabbit). Sukaryctas Metacoa, Chordera, Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. VCBI_TaxID=10090, 10116, 9986;
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EMBL, BC005269, AAH05269.1; -
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PDB, 1RCH, 28-NOV-01.
PDB, 1PLP, 31-JUL-95.
PDB, 1PLP, 33-JUL-95.
PDB, 1PSL, 03-JUN-95.
Genew, HGNC:9080; PLN.
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es 16; Conserv
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10-OCT-2003
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HSSP; P26678; 1PLP
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                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=Rabbit;
MEDIJNE=88112222; PubMed=2962883;
Fujii J., Lytton J., Tada M., Maclennan D.H.;
"Rabbit cardiac and slow-twitch muscle express the same phospholamban
                                                                                                             Fujii J., Zarain-Herzberg A., Willard H.F., Tada M., Maclennan D.H., "Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6."; J. Biol. Chem. 266:11669-11675(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in vitro.";

Circ. Res. 71:1021-1030(1992).

-!- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.
-!- SUBGNIT: Homopentamer.
-!- SUBCNIT: Homopentamer.
-!- SUBCNIT: Homopentamer.
-!- TISSUE SPECIFOITY: Heart.
-!- TISSUE SPECIFOITY: Heart.
-!- PPIM: Phosphorylated in response to beta-adrenergic stimulation.
-!- SIMILARITY: Belongs to the phospholamban family.
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Sharahan C.M., Weissberg P.L., Metcalfe J.C.;
"Isolation of gene markers of differentiated and proliferating
vascular smooth muscle cells.";
Circ. Res. 73:193-204(1993).
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SPECIES=Rat; TISSUE=Aortic smooth muscle;
MEDLINE=92206263; PubMed=1725098;
MHWANG K.S., Nadal-Ginard B.;
"Cloning phospholamban cDNA from rat aortic smooth muscle.";
Adv. Exp. Med. Biol. 304:387-395(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iochem. Biophys. Res. Commun. 188:927-933(1992).
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BMBL; M63500; -; NOT ANNOTATED_CD8.
EMBL; M63601; AAA31445.1; -.
EMBL; Y00761; CAA68730.1; -.
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SPECIES=Rabbit;
MEDLINE=91268032; PubMed=1828805;
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L03382; AAA41849.1; -. 895853; AAB21903.1; -. 895849; AAN86727.1; -. X71068; CAA50394.1; -.

EMBL; EMBL;

EMBL;

A49057; A49057. B40424; B40424. S37638; S37638.

PIR; PIR; PIR;

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POTENTIAL.
ACETYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
PHOSPHORYLATION (BY CAMK) (BY
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=C.familiaris; TISSUE=Heart ventricle;
MEDLINE=87316936; PubMed=3628007;
Uyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.;
"The cDNA sequence of the major phospholamban mRNA in canine cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=C.familiaris;
MEDLINE=86323152; PubMed=3753485;
Rujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
"Characterization of structural unit of phospholamban by amino acid sequencing and electrophoretic analysis.";
Biochem. Biophys. Res. Commun. 138:1044-1050(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Tada M., "Complete complementary DNA-derived amino acid sequence of canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cants tamiliaris (109).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodacryla; Suina; Suidae; Sus.
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SPECIES=C.familiaris;
MEDLINE=87008549; PubMed=3759968;
Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
Jones L.R.;
                                                                                                                                                                                                                          100.0%; Score 75; DB 1; Length 52; 100.0%; Pred. No. 1.3e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of phospholamban. Identification of phosphorylation sites and two major structural domains."; J. Biol. Chem. 261:13333-13341(1986).
MGD; MGI:97622; Pin.
InterPro; IPR005984; P lamban.
Pfam; PF0472; Phospholamban; 1.
TIGRFAMS; TIGR01294; P_lamban; 1.
TYANDREM 1 1 31 CYTOPLASNIC (POTENTIAL).
TRANSMEM 32 52 POTENTIAL.
MOD_RES 1 1 ACCEPTATION (BY SIMILARIA MOD_RES 16 16 PHOSPHORYLATION (BY PKA)
MOD_RES 17 17 PHOSPHORYLATION (BY CAMK)
                                                                                                                                                                           SIMILARITY).
0763601F76A854D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Cardiac phospholamban (PLB).
                                                                                                                                                                                                                                                                                                                                                                                                                        52 AA.
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MEDLINE=87083954; PubMed=3793929;
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J. Clin. Invest. 79:301-304(1987)
                                                                                                                                                                                                                                                                                                                    1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                1 MEKVOYLTRSAIRRAS 16
                                                                                                                                                                                           6094 MW;
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Best Local Simi
Matches 16;
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RL19 STRAW
Q82JW4;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                            SEQUENCE FROM N.A.
SPECIES-Pig; TISSUB-Smooth muscle;
MEDLINE=90056437; PubMed=2530978;
Verboomen H., Wuytack F., Eggermont J.A., de Jaegere S.,,
Wissiaen L., Raeymaekers L., Casteels R.;
"cDNA cloning and sequencing of phospholamban from pig stomach smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                               Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; "Phospholamban phosphorylation in intact ventricles. Phosphorylation of serine 16 and threonine 17 in response to beta-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                     Blocken, J. 262:353-356(1989).

-!- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.
-!- SUBGNAT: Homopentamer.
-!- SUBCELLULAR LOCATION: Membrane.
-!- TISSUE SPECIFICITY: Heart.
-!- PTM: Phosphorylated in response to beta-adrenergic stimulation.
-!- PTM: Phosphorylated in response to seta-adrenergic stimulation.
-!- SIMILARITY: Belongs to the phospholamban family.
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Transmembrane; Phosphorylation; Acetylation; 3D-structure.
DOMAIN 131 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 52;
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Pred. No. 4.9e-07;
1; Mismatches 0; Indels
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PHOSPHORYLATION (BY PKA).
PHOSPHORYLATION (BY CAMKI).
076361D9ADC424D3 CRC64;
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01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 AA
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                                                                                                                                                     Biol. Chem. 264:11468-11474(1989)
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93.8%; Prec.
      MEDLINE=89291905; PubMed=2544595;
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InterPro; IPR005984; P lamban.
Pfam; PF04272; Phospholamban; 1.
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EMBL; Y00399; CAA68461.1; --
EMBL; M35393; AAC41648.1; --
EMBL; X15075; CAA3171.1; --
PIR; A29002; A29002.
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Best Local Similarity
'-hes 15; Conserve
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NCBI_TaxID=9031;
[1]
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P26677
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                                                                                                                                                                                            phospholamban.";
J. Biol. Chem. 266:5375-5383(1991).

-.- FUNCTION: Phospholamban has been postulated to regulate the cartivity of the calcium pump of cardiac sarcoplasmic reticulum.
-.- SUBUNIT: Homopentamer.
-.- SUBCELLULAR LOCATION: Membrane.
-.- TISSUE SPECIFICITY: Heart.
-.- TISSUE SPECIFICITY: Heart.
-.- PTM: Phosphorylated in response to beta-adrenergic stimulation.
-.- SIMILARITY: Belongs to the phospholamban family.
SEQUENCE FROM N.A.
PEDIDINGUED-1170195;
TOYOFIUKU T., Zak R.;
"Characterization of cDNA and genomic sequences encoding a chicken "Characterization of cDNA and genomic sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

MEDLINE=21477403; PubMed=11572948;

Omuta S., Itakada H., Ishikawa J., Hanamoto A., Takahashi C.,

Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,

Kixuchi H., Shiba T., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ablility of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces avermitilis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
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PHOSPHORYLATION (BY PKA) (BY PHOSPHORYLATION (BY CAMK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.7%; Score 71; DB 1; Length 52; 87.5%; Pred. No. 7.6e-07; ive 2; Mismatches 0; Indels
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PIR; A39535; A39535.

HSSP, p26678, P1DLP.

InterPro; IPPR005984; P lamban.

Pfam; PF04272; Phospholamban; 1.

TIGRPAMS; TIGR01294; P lamban; 1.

Transmembrane; Phosphorylation; Acctylation.

Transmembrane; Phosphorylation; Acctylation.

ACTYPOPLASMIC (POTENTIAL).

51

POTENTIAL.

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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
50-MAR-2004 (Rel. 43, Last annotation update)
RPLS OR SAV2640.
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EMBL; M59038; AAA63167.1; -.
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Best Local Similarity
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SPECIES=S.lividans; STRAIN=TK21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
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                                                                                                     Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
"I FUNCTION: This protein is located at the 305-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
"I SINILARITY: Belongs to the L19P family of ribosomal proteins.
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SPECIES-S. COELICOLOR; STRAIN-A3(2) / M145;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Rapseger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.7%; Score 41; DB 1; Length 116; 46.7%; Pred. No. 1; ive 5; Mismatches 3; Indels
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InterPro; IPR01857; Ribosomal L19.
Pfam; PF01245; RIBOSOMĀLL19; I.
PRINTS; PR00061; RIBOSOMĀLL19.
ProDom; PD002979; Ribosomal L19; 1.
TIGRFAMS; TIGR01024; TpLS bact; 1.
PROSITE; PS01015; RIBOSOMĀLL19; 1.
Ribosomal protein; Complete proteome.
SRQUENCE 116 AA; 13186 MW; 47081773B07F6EB6 CRC64;
                                        STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902, 1916;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence by Son Free-2003 (Rel. 41, Last annotation update)
50S ribosomal protein Li9.
RPLS OR SCOSSES OR SCOSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SCOSSES OR SC
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81 VEKIELVTRGDVRRA 95
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SEQUENCE FROM N.A.
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Parro V., Mellado R.P.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
interface and may play a role in the structure and function of the
aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAINEATCO 35210 / B31;
STRAINEATCO 35210 / B31;
STRAINEATCO 35210 / B31;
STRAINEATCO 35210 / B31;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:580-586 (1997).

-!- FUNCTION: This protein is located at the 308-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).

-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
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EMBL; Z86111; CAA06800.1; -...
PTF; T43480; T34780.
HAMAP; MF 00402; -; 1.
InterPro; IPR001857; Ribosomal L19;
PFAm; PP01245; Ribosomal L19; 1.
PFDDm; PR00061; RIBOSOMALL19; 1.
PFDDm; PR00061; RIBOSOMALL19; 1.
RINTS; PR00161; RIBOSOMALL19; 1.
PROSITE; PS01015; RIBOSOMALL19; 1.
PROSITE; PS01015; RIBOSOMALL19; 1.
Ribosomal protein; Complete Protecme.
SEQUENCE 116 AA; 13142 MW; 37D782C6763D0A90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 116;
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L19.
RPLS OR BB0699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Pred. No. 1; 5; Mismatches
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                                                                                                                                                                                                                                                                             entities requires a license agreement (St or send an email to license@isb-sib.ch).
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Best Local Similarity 46.7%;
Matches 7; Conservative
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81 VEKIELVTRGDVRRA 95
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Gaps

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Length 871; 4; Indels

DB 1;

52.0%;

Query Match Best Local S Matches 9

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002138; tRNA-synt_2c.
InterPro; IPR006139; tRNA-synt_Ala.
Pfam; PF01411; tRNA-synt_C; 1.
PRINTS; PR00980; TRNASYNTHALA.
TIGRPAM6; TIGR00344; alas; 1.
PROSTIE; PS50860; AA TRNA_LIGASE II ALA; 1.
Aminpacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Rueps H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alanyl-RNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS)
ALAS OR TAN8849.
Thermoplasma acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.3%; Score 40; DB 1; Length 121; 53.3%; Pred. No. 1.7;
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Thermoplasmataceae; Thermoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein, Complete proteome.
SEQUENCE 121 AA; 14011 MW; A33F7B1E4DF24070 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                871 AA; 99907 MW; 6A6B5547846366D CRC64;
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InterPo; IPR001857; Riboscmal L19.
Fam; PF01245; Riboscmal L19; I.
FRINTS; PR00061; RIBOSCMALL19.
Pr000m; PD002979; Riboscmal L19; 1.
TIGRFAMS; TGGR01024; FD18 Dact; 1.
PROSITE; PS01015; RIBOSCWAL L19; 1.
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                                                                                                                                                                                                             PIR; B70187; B70187.
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SEQUENCE 871 AA
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Q9HJW4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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PSD CHLCV
OS21L3,
DT 10-0CT-2003 (Rel. 42, Last sequence update)
DT 10-0CT-2003 (Rel. 42, Last sequence update)
DT 10-0CT-2003 (Rel. 42, Last annotation update)
DT 10-0CT-2003 (Rel. 42, Last annotation update)
DT 10-0CT-2003 (Rel. 42, Last annotation update)
DT 10-0CT-2003 (Rel. 42, Last annotation update)
DT 10-0CT-2003 (Rel. 42, Last annotation update)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 1; Length 115;
Pred. No. 3.8;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AA; 13395 MW; 9EBE9A1B89D3122B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
550S ribosomal protein L19.
RPLS OR ITE1457.
Score 39; DB 1
Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                           115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERMY PF01245; Ribosomal L19; I. PRINTS; PR00061; RIBOSOMALL19. ProDom; PD002979; Ribosomal L19; 1. TGRPAMS; TIGRO1024; rplS bact; 1. PROSITE; PS01015; RIBOSOMĀL_L19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.0%;
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SEQUENCE 115 AA; 13395 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEKVQYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 LEKIEVIRKGKVRRA 94
                                                                                                                                                                                         353 KVGYLARMLIRRA 365
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Best Local Similarity 40...
6; Conservative
                                                                                                                           3 KVOYLTRSAIRRA 15
                                   Similarity 69.2
9; Conservative
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        RL19_THETN
                                                                                                                                                                                                                                                                                                                                                                        Q8R9X4;
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                                                                    Matches
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | || |:||::::
259 EDKQYFTQSAVKKSN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPOD OR XAC3788.
                                       NCBI_TaxID=714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XANAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08PG33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPSD_XANAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NONHYDROLYTIC) (BY SIMILARITY).
TO A PYRUVOYL GROUP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CTT-2003 (Rel. 42, Last annotation update)
18 Bis (S-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)
(Diadenosine tetraphosphatase) (Ap4A hydrolase) (Diadenosine 5',5''-
P1,P4-tetraphosphate pyrophosphoyrolase).
                                                                                                                                                                                                                                             "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
examining the role of niche-specific genes in the evolution of the
Chlamydiaceae.";

"Nucleic Acids Res. 31:2134-2147(2003).

-!- CATALYTIC ACTIVITY: Phosphatidyl-L.serine =
phosphatidylethanolamine + CO(2).

-!- COFACTOR: Pyruvoyl group (By similarity).

-!- SIMILARITY: Belongs to the phosphatidylserine decarboxylase
family. Subfamily 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN (BY SIMILARITY).
PHOSPHATIDYLSERINE DECARBOXYLASE ALPHA
CHAIN (BY SIMILARITY)
CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY
CONVERTED TO A PYRUVOYL GROUP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005221; PS_decarb.
Pfam; PF02666; PS_Dcarbxylase; 1.
TIGRFAMs; TICR00163; PS_decarb; 1.
Phospholipid biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHATIDYLSERINE DECARBOXYLASE BETA
                                                                                                                              STRAIN=GPIC;
MEDLINE-2566155; PubMed=12682364;
MEDLINE-2566155; PubMed=12682364;
Read T.D., Myers G.S.A., Burnham R.C., Nelson W.C., Paulsen I.T., Heidelberg J., Holtzapple B., Khouri H., Federova N.B., Carty H.A. Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
                                     Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83557;
Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine decarboxylase beta chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.7%; Score 38; DB 1; Length 299; 43.8%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
6F8EB837D97EE4E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP; MF 00663; -; 1.
InterPro; IPR003817; PS Dearbxylase.
InterPro; IPR002221; PS decarb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE016997; AAP05666.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 AA; 34223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
                                 PSD OR CCA00927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCA00927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APAH ACTAC
OS2655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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APAH_ACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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MEDLINE-22022145; PubMed=12024217;

A GLASSIVA A.C.R.; Ferro J.A.; Reinach F.C.; Farah C.S.; Furlan D.R.;

A Quaggio R.B.; Monteiro-Vitorello C.B.; Van Sluys M.A.; Almeida N.F.;

A Alves L.M.C.; do Amaral A.M.; Bertolini M.C.; Camargo L.B.A.;

A Cicarelli R.M.B.; Coutinho L.L.; Cursino-Santos D.R.; Ellopriy H.;

A Cicarelli R.M.B.; Coutinho L.L.; Cursino-Santos W.R.; Illorry H.;

A Taria J.B.; Ferraira A.J.S.; Ferrefra R.C.C.; Ferro M.I.T.;

A Paria J.B.; Ferraira A.M.; A.S.; Ferrefra R.C.C.; Gruber A.;

A Corali B.C.; Machado M.A.; Madeira A.M.B.N.; Martinez-Rossi N.M.;

A Moreira L.M.; Novo M.T.M.; Okura V.K.; Oliveira V.R.;

A Moreira L.M.; Novo M.T.M.; Okura V.K.; Oliveira W.C.; Oliveira V.R.;

A Pereira H.A.; Rossi A.; Sena J.A.D.; Silva C.; de Souza R.F.;

A Pereira H.A.; Rossi A.; Tamura R.B.; Teixeira B.C.; Tezza R.I.D.;

A Trindade dos Santos M.; Truffi D.; Tsai S.M.; White F.F.;
Saarela M., Fives-Taylor P.,
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- PONCTION: Hydrolyzes diadenosine 5',5''-Pl,P4-tetraphosphate to yield ADP (By similarity).
-!- CATALYTIC ACTIVITY: P(1),P(4)-bis(5'-adenosyl)tetraphosphate + H(2)O = 2 ADP.
-!- SIMILARITY: Belongs to the Ap4A hydrolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonas axonopodis (pv. citri).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 AA; 31480 MW; 0843F4FE11FF6DAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.3%; Score 37; DB 1;
40.0%; Pred. No. 15;
tive 6; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RNA polymerase sigma factor rpoD (Sigma-70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP, MF 00199; -; 1.
InterPro; IRR04647; ApaH.
InterPro; IRR004643; M-ppestrase.
InterPro; IRR006186; T_phtase_apaH.
Pfam; PR00149; Merallophos; 1.
Probom; P0000252; T_phtase_apaH; 1.
TIGRFAMS; TIGR00669; apaH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Setubal J.C., Kitajima J.P.;
"Comparison of the genomes of two Xanthomonas pathogens with differing host specificalities.";
Nature 417.459-463(2002).
-!- FUNCTION: The sigma factor is an initiation factor that promotes attachment of the RNA polymerase to specific initiation sites and then is released. This is the primary sigma-factor of this bacteria (By similarity).
-!- SIMILARITY: Belongs to the sigma-70 factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salvini M., Bini E., Santucci A., Batistoni R.,
"H4 histone in the macronucleus of Blepharisma japonicum (Protozoa,
"ilophora, Heterotithida).";
FEMS Microbiol. Lett. 149:93-98 (1997).
-!- FUNCTION: Histone H4.
-in nucleosome formation.
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Pram; Pr045542; sigma70_ri_1.
Pram; PP045545; sigma70_ri_1.
Pram; PF04555; sigma70_ri_1.
PROSTE; PS00046; SIGMA70FCT.
PROSTE; PS00715; SIGMA70_li_1.
Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
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Bukaryota; Alveolata; Ciliophora; Heterotrichea; Heterotrichida;
Blepharismides; Blepharisma.
NCBI_TaxID=5961;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; ABOLZO, AMANGOSO, I. InterPro; IPR009043; RNA pol sigma.

InterPro; IPR009043; RNA pol sigma.

InterPro; IPR007127; Sigma70 rer.

InterPro; IPR007042; Sigma70 rl.

InterPro; IPR007627; Sigma70 rl.

InterPro; IPR007627; Sigma70 rl.

InterPro; IPR007630; Sigma70 rl.

InterPro; IPR007630; Sigma70 rl.

InterPro; IPR00943; Sigma70 rl.

Pfam; PP00466; sigma70 rl.

Pfam; PP00409; Sigma70 rl.

Pfam; PP00140; Sigma70 rl.1;
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MEDLINE=97257506; PubMed=9103980;
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAIN=A5-3;
MEDLINE=9725766; PubMed=9103980;
Salvini M., Bini E., Santucci A., Batistoni R.;
Salvini M., Bini E., Santucci A., Batistoni R.;
Salvini M., Bini E., Santucci A., Batistoni R.;
"H4 histone in the macronucleus of Blepharisma japonicum (Protozoa, Ciliophora, Heterotrichida).";
FEMS Microbiol. Left. 149:93-98(1997).
-!- FUNCTION: Histone H4, along with histone H3, plays a central role in nucleosome formation.
-!- SUBUMIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
-!- SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146 bp of DNA.
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00047; HISTONE H4; PARTIAL.
Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
NON TER 97 97
                                                 Hiscone H4-1 (Fragment).
Blepharisma japonicum.
Bukaryota, Alveolata, Ciliophora, Heterotrichea, Heterotrichida,
Blepharismidae, Blepharisma.
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                                                                                                                                                                                                     Score 36; DB 1; Length 47;
Pred. No. 3.5;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 97 AA; 10722 MW; 64BBB2D65594607C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SiMILARITY: Belongs to the histone H4 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-46, AND SEQUENCE OF 9-97 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           H41 BLEJA STANDARD; PRT; 97 AA. P80737; P90815; 01-NOV-1997 (Rel. 35, Created) 25-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X97995; CAA66634.1; -.
InterPro; IPR007125; Hist TAF.
InterPro; IPR007125; Histome core_D.
InterPro; IPR001951; Histome_H4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00125, histone; 1.
PRINTS, PR00625, HISTONEH4.
Prodom; PD001827, Histone H4; 1.
SMART; SM00417; H4; 1.
                                                                                                                                                                                                           48.0%;
                                                                                                                                                                                                                         53.8%;
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ENIQGITKPAIRR 39
                                                                                                                                                                                                                           Local Similarity 53.8
nes 7; Conservative
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Best Local Similarity
Matches 7; Conserva
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RL19 COR Q8FP56;

RESULT 15 RL19 COREF

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                                                                                                                                       "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.", Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein is located at the 305-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P2C1 ARATH STANDARD, PRT; 434 AA.
P49597; 043717; 094C87;
01-FEB-1996 (Rel. 33, Created)
28-FEB-2003 (Rel. 43, Last annotation update)
Protein phosphatase 2C ABI1 (EC 3.1.3.16) (PP2C) (Abscisic acid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meyer K., Leube M.P., Grill B.;
"A protein phosphatase 2C involved in ABA signal transduction in
Arabidopsis thaliana.";
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MEDLINE=55007758; PubMed=7923358,
Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
"The A. thallana disease resistance gene RPS2 encodes a protein
containing a nucleotide-binding site and leucine-rich repeats.";
[31] 78:1089-1099(1994).
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           Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PRODOGI, RIBOSOMĀLLI9.
Probom: PD002979; Ribosomal L19; 1.
TIGRPAMS, TIGR01024; rplS bact; 1.
PROSITE; PS01015; RIBOSOMĀL L19; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 113 AA; 12875 MW; 2692B361BAFBA229 CRC64;
                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANT ASP-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF 00402; -; 1.
InterPro; IPR001857; Ribosomal L19.
Pfam; PF01245; Ribosomal_L19; I.
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MEDLINE=94255767; PubMed=8197457;
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80 IEKIEVIRRGDVRRA 94
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Science 264:1452-1455(1994)
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Best Local Similarity
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           à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. [13:1572-1579(2003).

-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacy1-tRNA binding site (By similarity).

-!- SIMILARITY: Belongs to the L19P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura B., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.;
                                                                                                                                                                                                                                                                                                          Corynebacterium efficiens.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 1; Length 113;
Pred. No. 9.1;
b; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9BD1C9D25ADA453A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                                                                                                                                (Rel. 43, Created)
(Rel. 43, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
SS ribosomal protein L19.
RPLS OR CGL2037.
                                                                                                                                                            113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP, MF 00402; -; 1.
InterPro_IPR001857; Ribosomal L19.
Pfan, PP01245; Ribosomal L19; 1.
PRINTS: PR001601; RIDOSOMALL19.
ProDom; PD002979; Ribosomal L19; 1.
TICRFAMS: TIGR01024; rp1s bact; 1.
PROSITE; PS01015; RIBOSOMAL_L19; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 113 AA; 13008 MW; 9BD1C9D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP005220; BAC18742.1; ALT_INIT.
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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ENIQGITKPAIRR 38
2 EKVQYLTRSAIRR 14
                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                50S ribosomal | RPLS OR CE1932
                                                                                                                                                                                                                  15-MAR-2004
15-MAR-2004
                                                                                                                                                                                             15-MAR-2004
                                                                                                                                                       COREF
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OBNNZ0;
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Query Match

Matches

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CORGL

RESULT 16
RL19\_CORGL
ID\_RL19\_CORGL
AC Q8NNZ
DT 28-FE
DT 28-FE
DT 28-FE
DT 28-FE
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CS REPLS
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MEDLINES. Columbia;
MEDLINES.22948E0; PubMed=14593172;
MEDLINES.22948E0; PubMed=14593172;
MEDLINES.22948E0; PubMed=14593172;
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlinn-Newmann G. Liu S.K., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L. Tipp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Ondera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
Choo Q., Choy N., Enju A., Goldanth A.D., Gurjal M., Hansen N.F.,
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
Khan S., Koeeema E., Ishida J., Jiang P.K., Jones T., Kawai J.,
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
                                                                                                                Arabidopsis ABA response gene ABI1: features of a calcium-modulated
                                                                   Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F.,
                        Columbia; TISSUE=Leaf;
                                            MEDLINE=94255766; PubMed=7910981;
                                                                                                                                                            Science 264:1448-1452(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 402:769-777(1999).
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
                                                                                                                                         protein phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SMOUSA; FEECU; 1.

PROSITE; PSO1018; FEF HAND; 1.

PROSITE; PSO1032; PPZC; 1.

PROSITE; PSO1032; PPZC; 1.

PROSITE; PSO1032; PPZC; 1.

PHYDROLASE; Magnesium; Manganese; Multigene family; Calcium-binding.

CA BIND 93 104 POLY-VAL.

DOWAIN 417 420 POLY-VAL.

VARIANT 180 180 G -> D (WILTY PHENOTYPE AND ABA-CONFLICT 24 G -> R (IN REF. 5).

CONFLICT 24 24 G -> R (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2ASA HUMAN STANDARD; PRT; 486 AA.

015372;
030-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, alpha isoform (PP2A, B subunit, B' alpha isoform) (PP2A, B subunit, B' alpha isoform) (PP2A, B subunit, RS alpha isoform) (PP2A, B subunit, RS alpha isoform) (PP2A, B subunit, RS alpha isoform) (PP2A, B subunit, PR61 alpha isoform) (PP2A, B
                                                                                                                          -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                      -!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.0%; Score 36; DB 1; Length 434; 43.8%; Pred. No. 39; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4A4C54F04195F572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            EMBL; ALC1186 (AR54831; --
EMBL; ALC11864; CAB79463.1; --
EMBL; ALC11864; CAB79463.1; --
EMBL; ALC1864; CAB79463.1; --
FIR; T04263; T04263.
HSSP: P35813; 1A6Q.
INTERPRO: IPR00120168; EF-hand.
INTERPRO: IPR001932; PP2C-11Ke.
INTERPRO: IPR001932; PP2C-1
SMART; SM00331; PP2C5 SIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Breast cancer;
MEDLINE=96064678; PubMed=7592815;
McCright B., Virshup D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 24 G
105 105 I
434 AA; 47505 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 MSAAEYLSKLAIORGS 411
                                                                                                                                                                                                                                                                                                                             EMBL, X78886, CAA55484.1, -.
EMBL, U12856, AAA50237.1, -.
EMBL, X77116, CAA54383.1, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEKVQYLTRSAIRRAS 16
                                                       Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                            phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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2ASA HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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.. 0

Xanthomonas campestris (pv. campestris). Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

Xanthomonadaceae; Xanthomonas

NCBI\_TaxID=340;

RPOD OR XCC3736.

10-OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) RNA polymerase sigma factor rpob (Sigma-70).

624 AA.

STANDARD;

RPSD XANCP Q8P4H2;

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                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: PP2A consists of a common heterodimeric core enzyme, composed of a 36 kDa catalytic subunit (subunit C) and a 65 kDa constant regulatory subunit (PR65 or subunit A), that associates with a variety of regulatory subunits. Proteins that associate with the core dimer include three families of regulatory subunits B (the R2/B/R55/B55, R3/B'/PR72/PR13/PR59 and R5/B'/B56 amilies), the 48 kDa variable regulatory subunit, viral proteins, and cell signaling molecules.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIPICITY: Widely expressed with the highest expression in heart and skeletal muscle.
-!- PTM: Phosphorylated on serine residues.
                                                                                      Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I., Merlevede W., Goris J., Hemmings B.A.;
"The variable subunit associated with protein phosphatase 2A0 defines a novel multimember family of regulatory subunits.";
Biochem. J. 317:187-194(1996).
                                                                                                                                                                                                                                  both nucleus and cytoplasm.",
J. Biol. Chem. 271:22081-22089(1996).
-!- FUNCTION: The B regulatory subunit might modulate substrate
selectivity and catalytic activity, and also might direct the
localization of the catalytic enzyme to a particular subcellular
                                                                                                                                                                                              McCright B., Rivers A.M., Audlin'S., Virshup D.M.; "The B56 family of protein phosphatase 2A (PP2A) regulatory subunits encodes differentiation-induced phosphoproteins that target PP2A to
"Identification of a new family of protein phosphatase 2A regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, 142373, AA037601.1;
PIR, 155449; 155449.
Genew, HGMC.9309; PPP2R5A.
MIM, 601643; -
GO, GO:0005737; C:cytoplasm; TAS.
GO; GO:0006601; F:protein phosphatase type 2A, intrinsic regu. . .;
InterPro; IPR002554; B56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E -> F (IN REF. 2; AA SEQUENCE)
H -> S (IN REF. 2; AA SEQUENCE)
R -> E (IN REF. 2; AA SEQUENCE)
D31407F7032A6D44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 486;
                                                  SEQUENCE OF 47-56; 129-132; 347-354; 448-462 AND 471-480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.0%; Score 36; DB
50.0%; Pred. No. 44;
tive 3; Mismatches
                                                                                                                                                                      PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
MEDLINE=96355607; Pubmed=8703017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Incerto, ....
Promy PF01603; B56, 1.
Phosphorylation, Multigene family.
S POLY-SER
           subunits.";
J. Biol. Chem. 270:26123-26128(1995).
                                                                             MEDLINE=96276417; PubMed=8694763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
54
451
486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                       compartment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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STRAIN-ATCC 33913 / NOPPB 528;

RA STRAIN-ATCC 33913 / NOPPB 528;

RA Garacto R.B. Dubfed=12024217;

RA Quaggio R.B. Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA Alves L.M.E., Cannavan F., Cardozo J., Chambergo F., Ciagina L.F.,

RA Alves L.M.S., Ferreira R.C.C., Ferreira D.F.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Stsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Stsuyama A.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira B.C., Tezza R.I.D.,

Rating E.C., Maddanis J., Menok C.F. M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira B.C., Tezza R.I.D.,

Ratindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

R. Schubal J.C., Kitajima J.P.;

R. "Comparison of the genomes of two Xanthomonas pathogens with differing

R. "Comparison of the sigma factor is an initiation factor that promotes

attachment of the RNA polymerase to specific initiation sites and

L. "FUNCTION: The sigma factor is an initiation factor that promotes

attachment of the RNA polymerase to specific initiation sites and

L. SIMILARITY: Belongs to the sigma-70 factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Pfam; PF03979; sigma70 nr 1.2; 1.
Pfam; PF00140; sigma70 rr 1.2; 1.
Pfam; PF04542; sigma70 rr 1.2; 1.
Pfam; PF04539; sigma70 rr 3; 1.
Pfam; PF04545; sigma70 rr 3; 1.
Pfam; PF04545; sigma70 rr 3; 1.
PF1075; PF00046; SiGMa70 rr 3; 1.
PROSITE; PS00716; SIGMA70 rr 1.
Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 POLYMERASE CORE BINDING (POTENTIAL).
502 H-T-H MOTIF (BY SIMILARITY).
69947 MW; 1F6C8CA093F7FLAF CRC64;
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InterPro; IPR007631; Sigma70_ner.
InterPro; IPR007121; Sigma70_r1_1.
InterPro; IPR007627; Sigma70_r1_2.
InterPro; IPR007627; Sigma70_r2_1.
InterPro; IPR007624; Sigma70_r2_1.
InterPro; IPR007634; Sigma70_r3_1.
InterPro; IPR007634; Sigma70_r4.
InterPro; IPR000943; Sigma 70_r4.
Pfam; PF04546; sigma70_ner; 1.
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DNA BIND
SEQUENCE
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
11-DCT-2003 (Rel. 42, Last annotation update)
Magnesium-chelatase subunit chlD (Mg-protoporphyrin IX chelatase) (Mg-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (In) Plant Gene Register PGR97-091.
-!- FUNCTION: Involved in chlorophyll biosynthesis; introduces a magnesium ion into protoporphyrin IX to yield Mg-protoporphyrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Masuda T., Nakayama M., Ohta H., Takayama K.-I.; subunit of "Cloning and sequencing of a chlb gene encoding a subunit of magnesium-chelatase from the cyanobacterium Synechococcus sp. PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- PATHWAY: Chlorophyll biosynthesis.
-:- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
-:- SIMILARITY: Contains 1 VMFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR0002035; Wag—Chelatse_chii.
InterPro; IPR0002035; WWF A.
Pfam; PF01078; Mg_chelatase; 1.
Pfam; PF01078; Mg_chelatase; 1.
SWART; SM00382; VWa; 1.
SWART; SM00382; VWa; 1.
PROSITE; PS50234; VWFA; 1.
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                                        2; Mismatches
             50.0%; Pred. No. 57;
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                                                                                                                                                                     357 MEKANYLTLAEIKDIS 372
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Matches 7; Conservative
                                                                                                        1 MEKVQYLTRSAIRRAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 ÉQIGYLVREAIR 278
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                                        8; Conservative
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(Rel. 34, I
(Rel. 43, I
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   Best Local Similarity
Matches 8; Conserv
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PS1142;
01-OCT-1996 (
01-OCT-1996 (
15-MAR-2004 (
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DVL2_XENLA
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Segment polarity protein dishevelled homolog DVL-2 (Dishevelled-2) (DSH homolog 2) (Xdsh). Starbus laevis (African clawed frog). Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sokol S.Y., Klingensmith J., Perrimon N., Itoh K.; "Dorsalizing and neuralizing properties of Xdsh, a maternally expressed Xenopus homolog of dishevelled."; pevelopment 121:1637-1647(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF6C9A1662DD7CEB CRC64;
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InterPro; IPR000591; DEP.
InterPro; IPR000339; Dishevell.
InterPro; IPR003351; Dishevelled.
InterPro; IPR003351; Dishevelled.
InterPro; IPR001158; Dishevelled_2.
InterPro; IPR001158; DIX.
InterPro; IPR001158; DIX.
InterPro; IPR001158; DIX.
InterPro; IPR001158; DIX.
IPR00377; Dishevelled; I.
Pfam; PP00577; Dishevelled; I.
Pfam; PP00578; DISHEVELLED.
PRNNTS; PR01762; DISHEVELLED.
PRNNTS; PR01762; DISHEVELLED.
PRNDT; SW00021; DEP; I.
SWART; SW00228; DEP; I.
PR0SITE; PS50841; DIX; I.
PROSITE; PS50841; DIX; I.
PROSITE; PS50841; DIX; I.
PROSITE; PS50106; PDZ; I.
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MEDLINE=95324391; PubMed=7600981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96017659; PubMed=7588081;
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DOMAIN 1 82
                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
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428
680
736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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DB 1; Length 736;

Score 36;

48.0%;

924 AA; 100253 MW; 0162C1591AF040AC CRC64;

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1 MEKVQYLTRSAIRRAS 16
         SEQUENCE
                                                               Query Match
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Matches
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-!- CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
-!- ENZYME REGULATION: Hexokinase is an allosteric enzyme inhibited by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: In vertebrates there are four major glucose-phosphorylating isoenzymes, designated hexokinase I, II, III and IV (glucokinase).
-!- SIMILARITY: Belongs to the hexokinase family.
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"Complete amino acid sequence of the type III isozyme of rat
hexokinase, deduced from the cloned cDNA.";
Arch. Biochem. Biophys. 285:365-370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferace, Kinase, Glycolysis, Allosteric enzyme, Repeat, DOM-binding, Membrane REGULATORY.

1 488 REGULATORY.

1 0 488 OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE
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                                 Indels
                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Hexokinase type III (BC 2.7.1.1) (HK III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL). (POTENTIAL).
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GLUCOSE-BINDING
GLUCOSE-BINDING
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      Pred. No. 69;
2; Mismatches
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InterPro; IPR001312; Hexokinase.
Pfam; PP03727; hexokinase; 2.
Pfam; PF00349; hexokinase; 2.
PRINTS; PR00475; HEXOKINASE.
ProDom; PD001109; HEXOKINASES; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91378267; PubMed=1897938;
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70.08;
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                       STANDARD;
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624 EYSTRSSIRR 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RNA;(N).
-!- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beta', and beta'.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lemieux C., Otis C., Turmel M.;
"Ancestral chloroplast genome in Mesostigma viride reveals an early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substrates.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
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Eukaryota, Viridiplantae, Streptophyta, Mesostigmatophyceae,
Mesostigmatales, Mesostigmataceae, Mesostigma.
NCBI_TaxID=41882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.0%; Score 36; DB 1; Length 1080; 43.8%; Pred. No. 1e+02; ive 6; Mismatches 3; Indels
       Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6)
, DB 1;
88;
                                                                                                                                                                                                                                                                                                                                                                   1080 AA
48.0%; Score 36; DB 61.5%; Pred. No. 88; iive 1; Mismatches
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INTECPEO; IPRO07641; RNA POL B.
INTECPEO; IPRO07641; RNA POL Rpb2 1.
INTECPEO; IPRO07642; RNA POL Rpb2 2.
INTECPEO; IPRO07642; RNA POL Rpb2 3.
INTECPEO; IPRO07641; RNA POL Rpb2 7.
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Nature 403:649-652(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20150907; PubMed=10688199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF166114; AAF43826.1; -.
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                                                                      Conservative
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les 8; Conserv
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P10932;
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RA Amanatides P.G., Scherer S.E., 12 P.W., Hoskins R.A., Galle R.F.,

B. G., Scherer S.E., Rabburner M. Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chan L.X.,

B. Brandon R.C., Baxter E.G., Helf G., Changen M., Pfeiffer B.D.,

RA Abril J.F., Apdravani A., An H.-J., Andraves Pennikoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Burtis K.C., Busam D.A., Bulker J., Eddieu E., Center A., Chandra I.,

R. Abrill S.D., Delchan M. Bouck J., Brokerein P., Brotter P.,

Burtis K.C., Busam D.A., Buller H., Gadieu E., Center A., Chandra I.,

R. Abrill S.D., Delchar A., Dennes M., Down I. Dietz S.M.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

R. Abrill M. J., Harvey D. A., Henhan T.J., Hernandez J.R., Houck J.,

R. Abrill M. J., Harvey D. D.A., Henhan T.J., Hernandez J.R., Houck J.,

R. Alaush F., Kadrea C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

R. Alaush F., Kadrea C.D., Kraft C., Morris J., Moshrefi A.,

R. Muntle B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,

R. Mount S.M., Nelson K.A., Howland T.C., Morris J., Moshrefi A.,

R. Mount S.M., Nelson K.A., Howland T.C., Morris J., Moshrefi A.,

R. Mantei B. M., Nelson K.A., Moshrefi M., Stupski M.P., Smith T.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Santh T.,

Shue B.C., Shen H., Worley K.C., Wu D., Yang S., Yao Q.A.,

Walliams S.M., Woodage T., Wurley K., Wu D., Yang S., Yao Q.A.,

Walliams S.M., Wassarman D.A., Weiter J.C., Scheeler F., Shen H.,

R. Alberson S.M., Woodage T., Wu D., Wang S., Zhu X., Smith H.O.,

Glabbs R.A., Myers B.W., Rubin G.M., Weiter J.C., Shen H., Schener B., Rubins G., Cheller E., Shen H., Shener B., Shener B., Shener B., Rubins G., Shen B., Shener B., Shener B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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MEDLINE=22426066; PubMed=12537569;
MEDLINE=22426066; PubMed=12537569;
MEDLINE=22426066; PubMed=12537569;
MEDLINE=22426066; PubMed=12537569;
MIN, Carlson J.W., Brokstein P., Yu C., Champe M.,
Rubin G.M., Calniker S.E.;
Rubin G.M., Celniker S.E.;
Ma Drosophila full-length CDNA resource.";
Genome Biol. 3:RBSEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hekapoda, Insecta, Pterygota, Neoptera, Endopteryapota, Diptera, Brachycera, Muscomorpha; Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
60s ribosomal protein L28.
                                                                                                                                                                                                                                                                144 AA.
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66 LKRPKYNERTSIRRAS 81
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MEDLINE=99437995; PubMed=10508151;
O'Hara B.P., Norman R.A., Wan P.T., Roe S.M., Barrett T.E., Drew R.E.,
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STRAINS-ATC 15692.
PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.C., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Alckey M.C., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Brody L.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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"Nucleotide sequence of the aliphatic amidase regulator gene (amiR)
of Pseudomonas aeruginosa.";
FEBS Lett. 246:39-43(1989).
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Wilson S.A., Drew R.E.;
"Transcriptional analysis of the amidase operon from Pseudomonas
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Pseudomonadaceae, Pseudomonas
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Aliphatic amidase regulator.
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ProDom; PD010767; Ribosomal L28e; 1.
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Nature 406:959-964(2000).
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         "Crystal structure and induction mechanism of Amic-AmiR: a ligand-regulated transcription antitermination complex."; EMBO U. 18:5175-5186(1999).
-!- FUNCTION: Positive controlling element of amiE, the gene for aliphatic amidase. Acts as a transcriptional antitermination factor. It is thought to allow RNA polymerase read through a rhoindependent transcription terminator between the amiE promoter and
                                                                                                                                                                                                          EMBL, X13776; CAA32023.1; --
BMBL, AB004758; AAG06751.1; --
PIR, B83226; B83246
PIR, B8326; B8326.
PIR, S03884; S03884; S03884; S03884; S03884; S03884; S03884; S03884; S03884; S03884; S03884; S03884; SPRSF035581; ANTAR.
InterPro; IPR00327; Res_reg_antiterm.
Pfam; PF03861; ANTAR; 1.
PIRSF; PIRSF036382; Res_reg_antiterm; 1.
Transcription regulation; Transcription antitermination; 3D-structure;
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Query Match
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Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 3; Indels

Search completed: October 1, 2004, 12:18:18 Job time: 9.8 secs

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Q99zw6 streptococc Q8p177 streptococc Q87zb1 streptococc Q87zb5 streptococc Q94sq7 oryza sativ Q8dj60 synechococc Q91sb synechococc Q91sb synechococc Q91sb synechococc Q7uwm3 rhodopirell

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Q8yw91 anabaena sp
Q92ry5 rhizobium m
Q9nwf6 homo sapien
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STRAIN=MA-4680 N.A.:

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MEDLINE=22608306, PubMed=12692562;

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MEDLINE=22608306, PubMed=12692562;

MIKeda H., Ishikawa J., Haramoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., Shinose M., Kikuchi H., Shiba T., Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";

MIL. Biotechnol. 21:226-531 (2003).

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MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria, Actinobacteridae, Actinomycetales;
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
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46.7%; Pred. No. 7.5;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ribosomal protein 119.
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Q92RY5
Q9NWF6
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PROSSITE; P801015; RIBOSOMAL_L19; 1
Ribosoma; protein; Complete protes
SEQUENCE 116 AA; 13186 MW; 470
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                                                                                                           Streptomyces avermitilis.
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MEDLINE-20141373; PubMed=10675398;

Fazeli C.F., Rezadan M.A.;

Fazeli C.F., Rezadan M.A.;

Fux clockide sequence and organization of ten open reading frames in the genome of Grapevine leafroll-associated virus 1 and identification of three subgenomic RMAs.";

J.G. three subgenomic RMAs.";

G. GO.003723; R:RNA binding; IEA.

GO; GO.0003723; F:RNA binding; IEA.

GO; GO.0003650; P:transcription; IEA.

GO; GO.0019079; P:viral genome replication; IEA.

InterPro; IBR001788; RNA_dep_RNApol2.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
Ampelovirus.
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                                                          09UZT5;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                                                                                                Phospho-sugar mutase.
PYRAB10610 OR PAB1666.
Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-GE5 / Orsay;
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SEQUENCE 451 AA
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NCBI_TaxID=29292;
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Q9UZTS
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Matches
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Hypothetical protein; Complete proteome.
SEQUENCE 1104 AA; 125574 MW; 61C89EE3AB30C5DD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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01-JAN-1999 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus horikoshii,
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AC 058310;
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STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=125220739;
MARXIND K., OShima W., Kurokawa K., Vokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakaro M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                   53.3%; Score 40; DB 12; Length 527; 80.0%; Pred. No. 59; 1; Indels ive 1; Mismatches 1; Indels
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Vibrionaceae, Vibrio.
NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013626; AAH13626.1;
InterPro; IPR008160; Collagen.
Pfam; PF01391; Collagen; 12.
                                                                                                                                       527 AA; 59276 MW; C445CE1169B46132 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    998 AA; 95451 MW; ZAB4BA953B7084A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      998 AA
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InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PSvir.
PFam; PF00978; RNA_dep_RNApol_2; 1.
RNA-directed RNA_polymerase.
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EMBL; AP005088; BAC62605.1; -
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                                                                                                                                                                                          Query Match 53.3
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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95 QYVVRSAIRR 104
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Q8CFM4
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RO, GO:0005624; FILO4 binding; IEA.

RO, GO:0005624; FILOA binding; IEA.

RO, GO:0005624; FILOA binding; IEA.

RO, GO:0005624; FILOA binding; IEA.

RO, GO:0005624; FILOA binding; IEA.

RO, GO:0005627; FILOA replication initiation; IEA.

RO, GO:0005627; FILOA replication initiation; IEA.

RO, GO:0006542; INTEIN.

RO, GO:0006393; MCM. 2.

RINTERPRO; IPRO01208; MCM. 2.

RINTERPRO; IPRO01208; MCM. 2.

RR FAINTS; PRO0431; MCM. 2.

RR FAINTS; PRO0431; MCM. 2.

RR FAINTS; PRO0431; MCM. 2.

RR FAINTS; RR00306; HINCK; 2.

RR FAINTS; MR00306; HINCK; 2.

RR SMART; SM00306; HINCK; 2.
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           Length 1104;
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1108 AA; 125967 MW; 92D2578B31351F75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
01-274-1999 (TrEMBLrel. 09, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
1108AA long hypothetical cell division control protein.
Query Match 53.3%; Score 40; DB 16; L
Best Local Similarity 42.9%; Pred. No. 1.3e+02;
Matches 6; Conservative 6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1108 AA.
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Gaps

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"Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."; Submitted (UTL-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AJ748284; CA4494417.1; -. PIR; B75167; B75167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PYRAB04950.
PYRAB04950 OR PAB0314.
Pyrococcus abyssi.
Archaea, Euryarchaeota, Thermococci; Thermococcales; Thermococcaces;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Desulfovibrio desulfuricans.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
Desulfovibrionaceae; Desulfovibrio.
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Ringbauer J.A. Jr., Wall J.D.;
Ringbauer J.A. Jr., Wall J.D.;
Ringbauer J.A. Jr., Wall J.D.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR3131719; ARK11625.1; -..
RISSP; P00193; IDUR.
R GO, GO.0005189; F:electron transporter activity; IEA.
R GO, GO.0005189; F:electron transport, IEA.
R InterPro; IPR001450; 4Fe4S_ferredoxin.
R InterPro; IPR00106; Fe hydrog.
R InterPro; IPR00106; Fe hydrog.
R Ffam; PPR0037; fer4; 2.
R Ffam; PPR0037; fer4; 2.
R Ffam; PR00198; FePREDOXIN; 2.
R FFAM; PR0198; FePES_FERREDOXIN; 2.
R FFAM; PROITE; Iron; Iron-sulfur.
S SEQUENCE 421 AA; 46120 MW; 1116557AB0C94219 CRC64;
       Score 39; DB 16; Length 406;
Pred. No. 70;
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                                                       Indels
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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75.0%;
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NCBL_TaxID=29292;
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                 Query Match
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Q9V1D2;
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Q9AM36
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SEQUENCE FROM N.A.
STRAIR=SF370 / ATCC 700294 / Serotype M1;
MEDLINE=21192684; PubMed=11296296;
MEDLINE=21192684; PubMed=11296296;
Ferretti J.G., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
BMBL, AB005012, ARX3342.1;
Hypothetical protein; Complete proteome.
SEQUENCE 364 AA; 41754 MW, 038BBD36F4234020 CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
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EMBL; AE016781; AAN67537.1; -.
TICR; PP1920; --
TICR; PP1920; --
Hypothetical protein; Complete proteome.
SEQUENCE 406 AA; 47318 MW; 7CD8C30DF0D3C5E2 CRC64;
                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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(Tremblrel. 17, Last sequence update)
(Tremblrel. 19, Last annotation update)
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668 MEVKDYLTREEVRKA 682
MEKVOYLTRSAIRRA 15
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Best Local Similarity 53.8.
The Conservative
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A Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J. Adredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hang L., Kaegle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Carcio G. G., Mao J.-I., Rice P., Noelling J., Reeve J.N.; T. Complete genome sequence of Methanobacterium thermoautotrophicum of the Lath. functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155 (1997).

B. EmBL; ABG00827; AAB84931.1; -.

B. GO; GO:0005198; F: Structural molecule activity; IEA.

GO; GO:0005198; F: Structural molecule activity; IEA.

GO; GO:0007198; F: Structural molecule activity; IEA.

GO; GO:0007198; P: Structural molecule activity; IEA.

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MEDINE=21456156; PubMed=11572479;

MEDINE=21456156; PubMed=11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A. Aoki K.-I., Masuda S., Yangii M., Nishimura Y., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobus tokodaii.
Archaea, Crenarchaeota, Thermoprotei; Sulfolobales, Sulfolobaceae;
Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.7%; Score 38; DB 17; Length 119; 37.5%; Pred. No. 29; ive 6; Mismatches 4; Indels
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DNA Res. 8:123-140(2001).
EMBL, PAD00983, BAB65618.1;
InterPro; IPR003301; UCP016498.
Hypothetical proctein; Complete proteome.
SEQUENCE 122 AA; 14467 MW; 988A31A274842EB3 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein ST0620.
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Pred. No. 30;
5; Mismatches 3;
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          STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
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26 MKKIKYLTEEALMK 39
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MEDLINE=2255937; PubMed=12674476;
MEDLINE=2255397; PubMed=12674476;
Kloetzel J.A., Barcin-Tourancheau A., Miceli C., Barchetta S.,
Farmar J., Baneriee D., Fleury-Aubusson A.;
"Plateins: a novel family of signal peptide-containing articulins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Euplotes aediculatus:
Bukaryota: Alveolatus: Ciliophora; Spirotrichea; Hypotrichia;
Euplotida: Euplotidae; Euplotes.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005267; F:potassium channel activity; IEA.
GO; GO:0006813; P:potassium ion transport; IEA.
InterPro; IPRO1622; K-channel porte;
Hypothetical protein; Complete proteome.
SEQUENCE 481 AA; 55655 MW; 685FE30056A45259 CRC64;
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7298E314EFB7417A CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Eukaryot. Microbiol. 50:19-33(2003)
EMBL; AY124991; AAM94464.1; -.
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74972 MW;
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                                                                                                                                                                                                                                                                  2 EKVQYLTRSAIRRA 15
                                                                                                                                                                                                                                                                                                                38 EKIKYIKRRAFERA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.5
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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PubMed=12615971;
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Matches 6; Conserv
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watenabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Mateumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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MEDINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
"Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DAN Res. 9:189-197(2002).
EMBL, AP005955: BAC50746.1; -.
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                                                                                                                                                                           Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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Pred. No. 53;
2; Mismatches 1; Indels
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Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL. BX294147; CAD78621.1; -
Kinse: Transferaes; Complete proteome.
SEQUENCE 211 AA; 23976 MW; 2FF54BF18F094376 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AA; 22494 MW; E461C88B14783C7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Thymidine kinase Tdk (EC 2.7.1.21).
                                                                                                        Last sequence update)
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72.7%;
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                                                                            01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, Bl15481 protein.
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Best Local Similarity 72...
Best Local Similarity 72...
8; Conservative
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Best Local Similarity 37.55
Matches 6, Conservative
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                                             PRELIMINARY;
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Q7UFR1
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TRAINSETTO / ATCC 700294 / Serctype M1;

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM INSERTING PROBLEM AND SECULORS.

RA STEALNSETTO / ATCC 700294 / Serctype M1;

RA PETTELLI J.G., McGhan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

RA PETTELLI J.G., McGhan W.M., Ajdic D.J., Savic D.J., Lin S.P.,

RA PETTELLI J.G., McGhan W.M., Ajdic D.J., Savic D.J., Lin S.P.,

RA PETTELLI J.G., Najar F.Z., Ren Q., Zhu H., Song L., Wnite J.,

RA Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., Wnite J.,

RA Wan X., Clifton S.W., Roe B.A., McLaughlin R.,

ROMDIECE Ganome sequence of an M1 strain of Streptococcus pyogenes.";

RT "Complete: Ganome sequence of an M1 strain of Streptococcus pyogenes.";

REMEL, AE006549; AAX33932.1;

ROM GO: GO: 000779; Prorphyrin Diosyntheels; IEA.

RG: GO: 0016491; F: coproporphyrin piosyntheels; IEA.

RG: GO: GO: 000779; Prorphyrin biosyntheels; IEA.

RG: GO: GO: 000779; Prorphyrin biosyntheels; IEA.

RICEPRO; IRRO0459; HemN rel.

RICEPRO; IRRO0459; Radical SAM;

RTGREMS; PRO4055; Radical SAM;

RTGREMS; TICRO0539; HemN rel;

RTGREMS; TICRO0539; HemN rel;

RTGREMS; TICRO0539; HemN rel;

RTGREMS; TICRO0539; HemN rel;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Wendland J., Philippsen P.;

Wendland J., Philippsen P.;

"Isolation and characterization of the Ashbya gossypii BUD3 gene.";

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF210625; AAG41241.1;

NON TER 252 252
                                                                                                                                                                                                       Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Ashbya.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.7%; Score 38; DB 3; Length 252; 54.5%; Pred. No. 66; 1; Indels tive 4; Mismatches 1; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative coproporphyrinogen III oxidase (EC 1.3.3.3)
HEMN OR SPY1040.
                                            Last sequence update)
Last annotation update)
    Created)
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
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2 EKVQYLTRSAIRRAS 16

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STRAIN-MGAS315 / Serotype M3;
MEDINE=22133808; PubMed=1212206;
MEDINE=22133808; PubMed=1212206;
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 398;
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                                                                                             Query Match 50.7%; Score 38; DB 16; Length 39
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pyogenes (serotype M3).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus agalactiae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Pfam; PF04055; Radical_SAM; 1.
SEQUENCE 398 AA; 45841 MW; 669A0563D1206261 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Putative coproporphyrinogen III oxidase.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
DeoR regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                      408 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                           124 EKIAVLQRSAVNRIS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 EKIAVLQRSAVNRIS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                     2 EKVOYLTRSAIRRAS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEMN OR SPYM3 0673,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=198466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=1311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  emergence.";
                                                                                                                                                                                                                                                                                                                                                                                                   Q8K7R5
ID Q8K7R5
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Q9F8B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MGAS8222 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18 group A streptococcus strains associated with acute rheumatic fever outbreaks.";
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BMBL, AE010030; AAL97657.1; -.

GO, GO:0004109; F:coproporan, IEA.

GO, GO:0004109; F:coproporphyrinogen oxidase activity; IEA.

GO, GO:0006779; P:coproporphyrinogen oxidase activity; IEA.

InterPro; IPR004559; HemN. rel.

InterPro; IPR004559; HemN. rel.

INTERFAMS; TIGR00539; hemN. IEA.

INTERFAMS; TIGR00539; hemN. rel; I.

Complete proteone; Hypothetical protein.

SEQUENCE 376 AA; 43093 MM; 7236F821EEB5EEE5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes (serotype M18).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae,
                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UJV-2003 (TrEMBLrel. 24, Last annotation update)
Putative coproporphyrinogen III oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative coproporphyrinogen III oxidase.
                                                                                                                                                                                    376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 AA.
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                                                                                                                                                                                    PRT;
                             102 EKIAVLORSAVNRIS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 EKIAVLORSAVNRIS 116
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus.
NCBI_TaxID=186103;
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                                                                                                             RESULT 18
Q8P177
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10878L1
10 01-01
DT 01-01
DT 01-01
DE PUTAT
DO STREP
ON STREP
ON STREP
ON STRAIP
RP SEQUE
RP STRAIP
RP STRAIP
RP AMAXAG
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Gaps .; 0

Query Match

Matches

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Gloeckner G., Elchinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A., "Sequence and analysis of chromosome 2 of Dictyostellum discoideum."; Nature 418:79-85(2002).
                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to Homo sapiens (Human). similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c,
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80.0%; Pred. No. 3.6e+02;
.ive 1; Mismatches 1; Indels
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005677; F:DNA binding; IEA.
InterPro; IPR001005; Myb DnA, binding.
InterPro; IPR001005; Myb DnA, binding.
InterPro; IPR0010673; S mold repeat.
Pfam; PF00526; S mold repeat; 13.
SMART: SM00717; SANT; I.
PROSTIE; PROSTIE; PROSTOSO90; MYB 3; 1.
SEQUENCE 1223 AA; I36240 MW; B7D92B2925F39C72 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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NCBI TaxID=32046;
                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Ferredoxin-dependent glutamate synthase.
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MEDLINE=22225144; PubMed=12240834;
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Best Local Similarity
'... '8, Conserv?
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                             Lachenauer C.S., Creti R., Michel J.L., Madoff L.C.,
"Mosaicism in the alpha-like protein genes of group B streptococci.",
Proc. Natl. Acad. Sci. U.S.A. 97:9630-9635 (2000).
-!- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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SEQUENCE FROM N.A.
BUTALIANCE, Nipponbare,
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Haiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
Mhite O., Salzberg S.L., Fraser C.M.,
"Oryza sativa chromosome 3 BAC OSJUBDO047D08 genomic sequence.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  EMBL, AF248038; AAG09976.1; -. OCCUPATION OF THE CONTROL OF CONTROL OF ELEMBER OF CONTROL OF ELEMBER OF CONTROL OF ELEMBER OF CONTROL OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF CONTROL OF ELEMBER OF ELEMBER OF CONTROL OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBER OF ELEMBE
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56.2%; Pred. No. 2.5e+02;
tive 2; Mismatches 5; Indels
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EMBL, AC137925, AAO73264.1; -- Hypothetical protein.
Hypothetical protein.
SEQUENCE 882 AA; 96573 MW; 5CDCB01A2569CEC0 CRC64;
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PROSITE; PS00894; HTH DEOR FAMILY; 1.
DNA-binding; Transcription; Transcription regulation.
SEQUENCE 578 AA; 66770 NW; CIDE74FBS943B8E3 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein OSJNBb0047D08.27.
OSJNBB0047D08.27.
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    MEDLINE=20402586; PubMed=10944228;
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Best Local Similarity 56.23
Best Local Similarity 56.23
Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                   Rhodopirellula baltica.
Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales,
Planctomycetaceae, Pirellula.
NCBL_TaxID=117;
                                                                                                                    Query Match 50.7%; Score 38; DB 16; Length 1541; Best Local Similarity 53.3%; Pred. No. 4.6e+02; Matches 8; Conservative 2; Mismatches 5; Indels (
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50.0%; Score 37.5; DB 16; Length 68;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 10; Conservative 3; Mismatches 1; Indels 1
InterPro, IPR006981; Glu_synth_NTN.
Pfam; PP01645; Glu_synthase; 1.
Pfam; PP01645; Glu_synth NTN; 1.
Pfam; PP04899; Glu_synt_Central; 1.
Pfam; PP01493; GxGxG; T.
Complete proteome.
SEQUENCE 1541 AA; 168017 MW; 9CB26077859306A6 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
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Hypothetical protein.
                                                                                                                                                                                                                                                                                       68 AA.
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